FIGURE 1

Chimeric blend A   Chimeric blend B

pH   5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 5.0 7.0 7.5 8.0 8.5 9.0 9.5 10.0 M
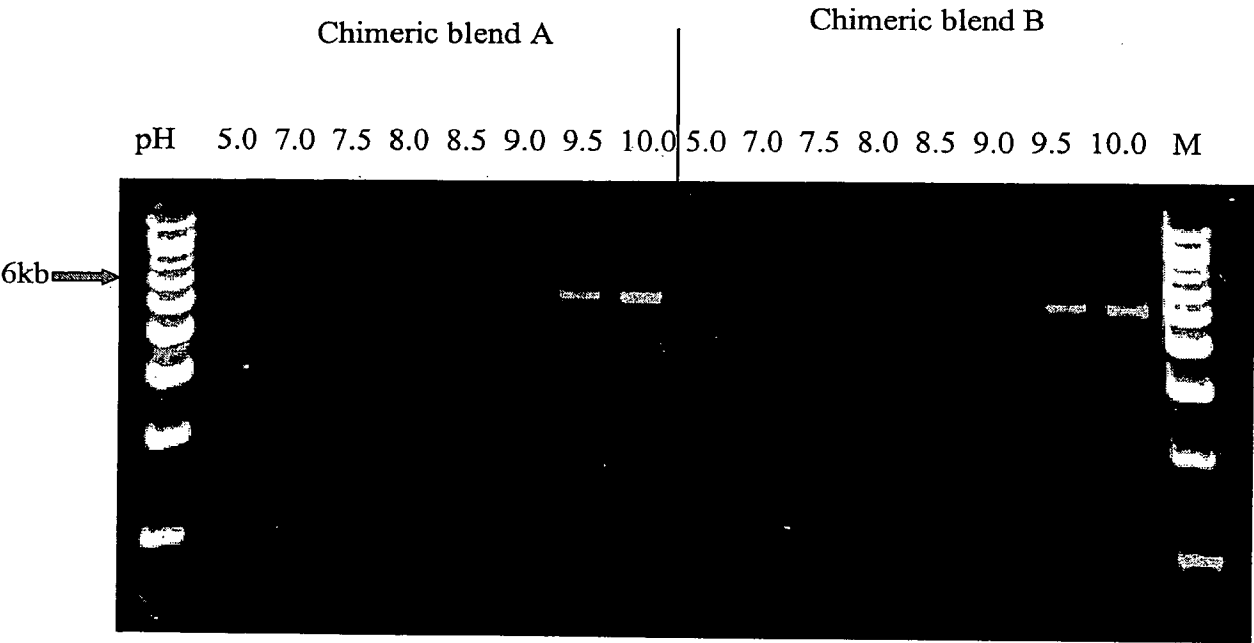
6kb

FIGURE 2

6kb BG
15"/kb - 1'-30"

1X Cloned buffer

FIGURE 3

19kb BG
30"/kb – 9.5' extension
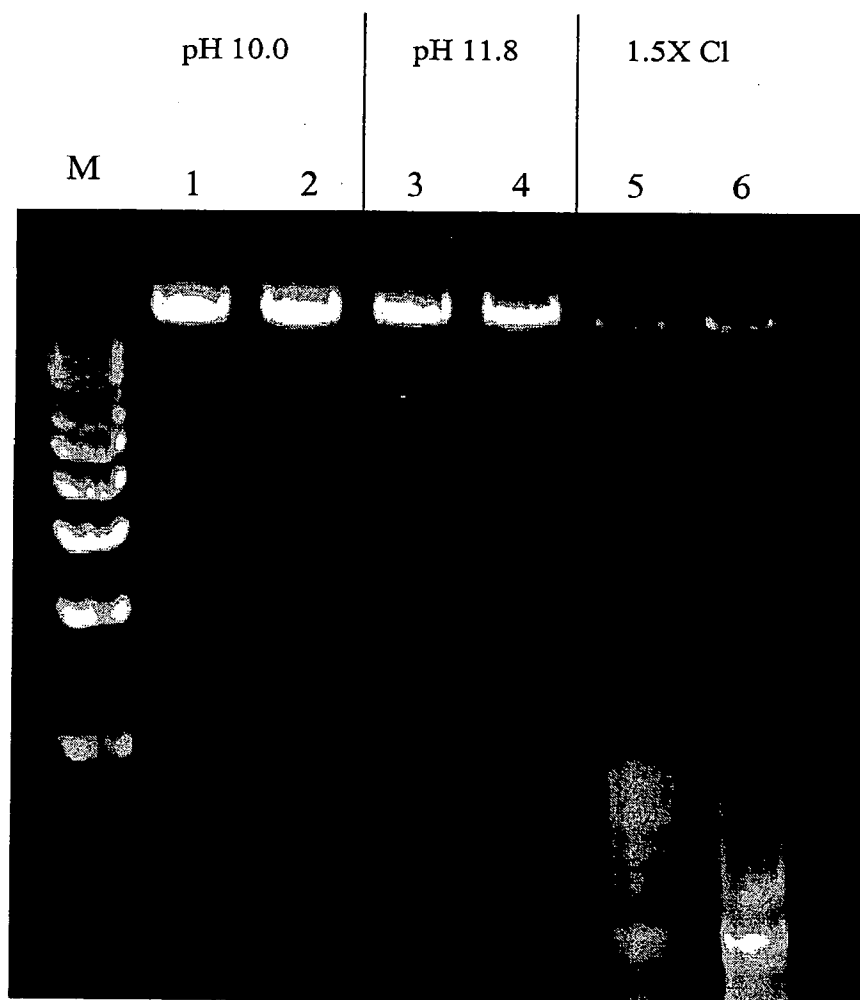
FIGURE 4

**19kb BG
30"/kb – 9.5' extension**

| | Pfu-Sso7d blend pH10.0 | | Pfu-Sso7d pH 10.0 | | Herculase | | Herculase 3%DMSO | |
| M | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |

19kb →

FIGURE 5

19kb BG
30"/kb - 9.5' extension
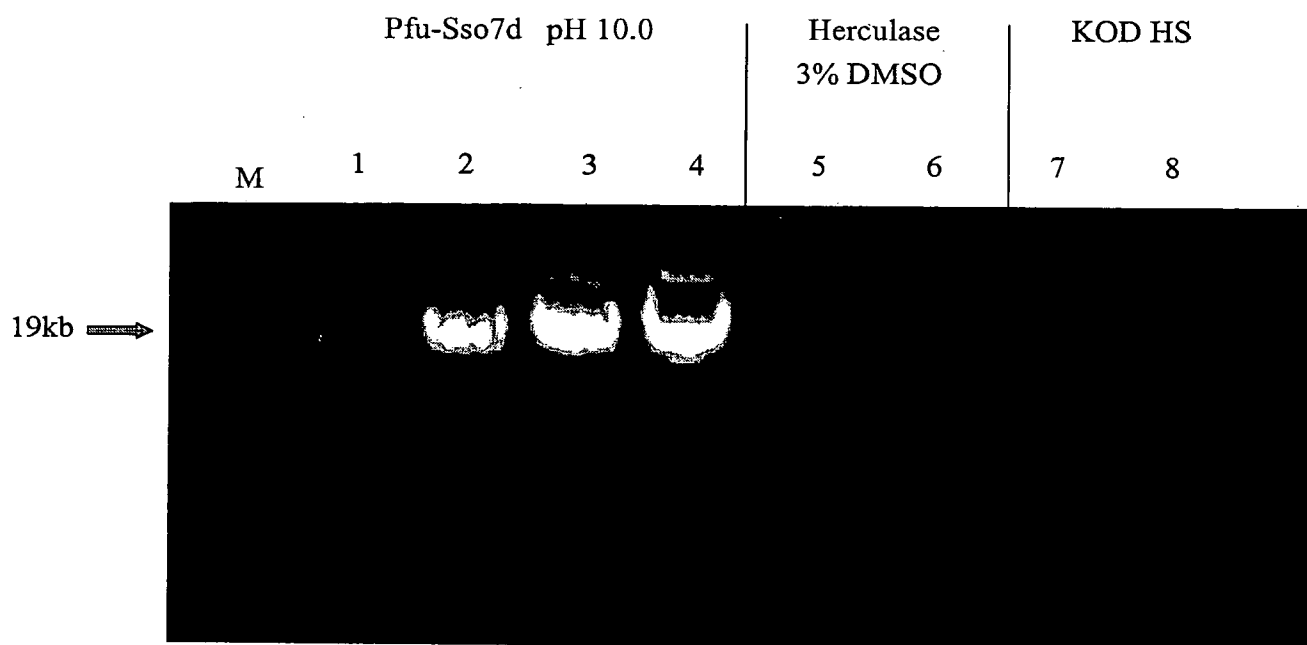
FIGURE 6
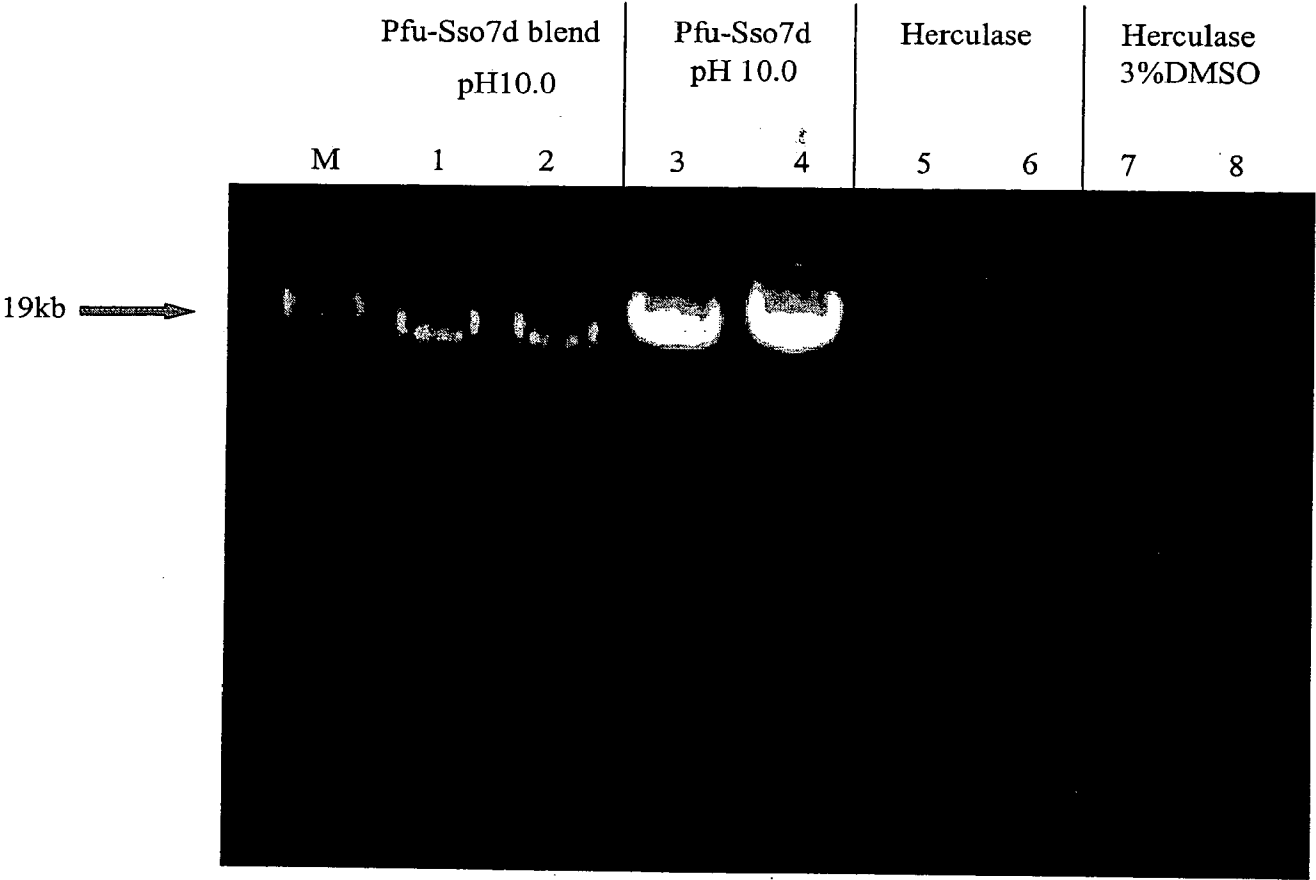
**900bp HαAT
1"/kb - 1" extension**
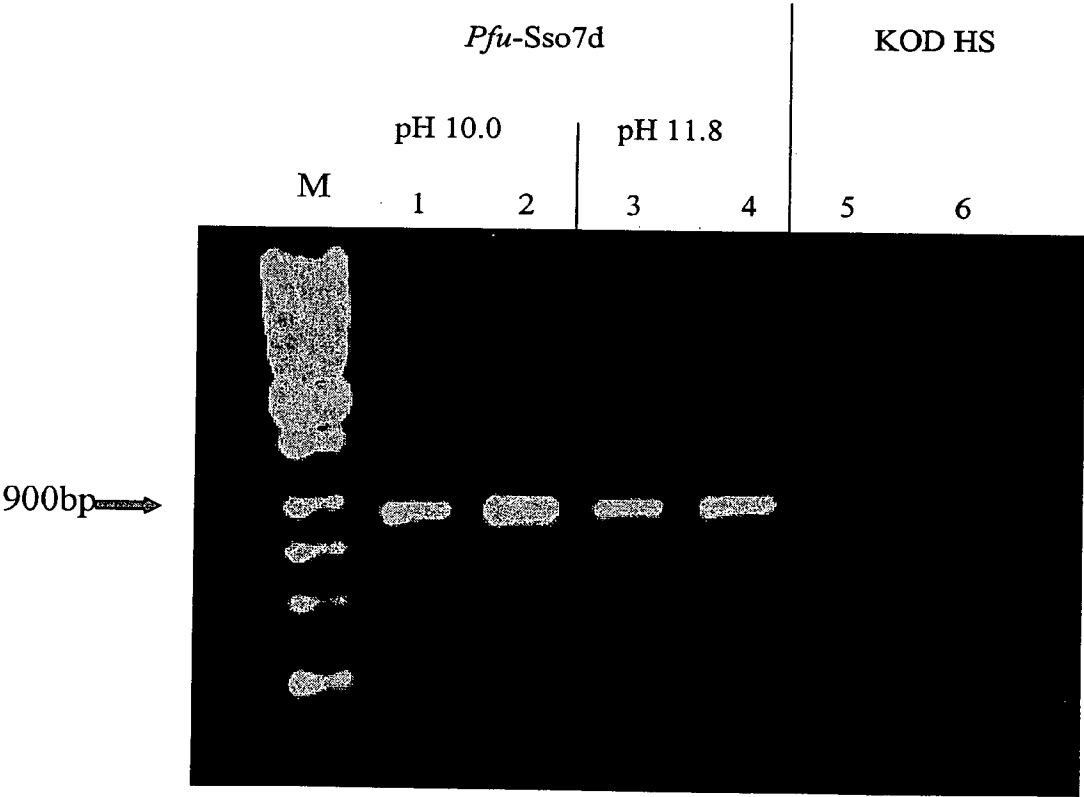
FIGURE 7

2.6kb HαAT
2"/kb - 5" extension

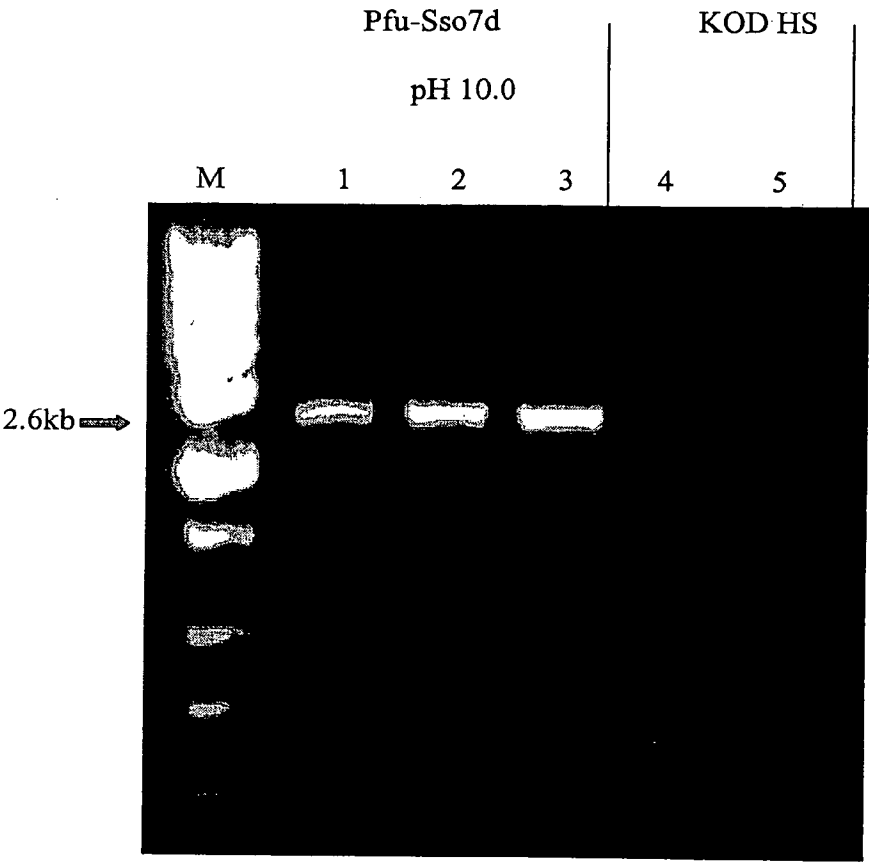FIGURE 8

**6kb BG
10"/kb – 1' extension**
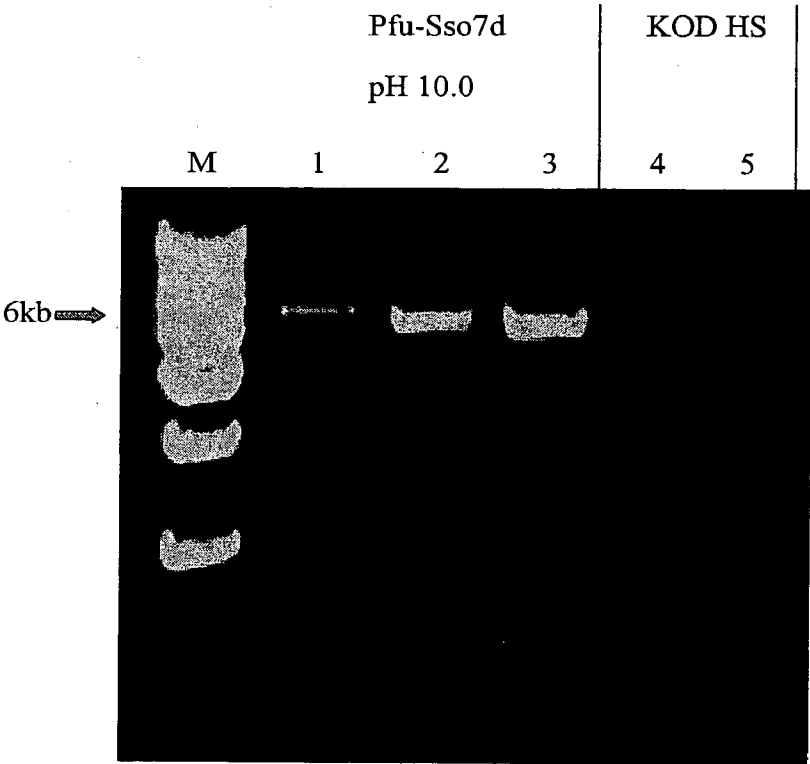
FIGURE 9

**2.6kb HαAT
30"/kb – 1'. 18" extension**
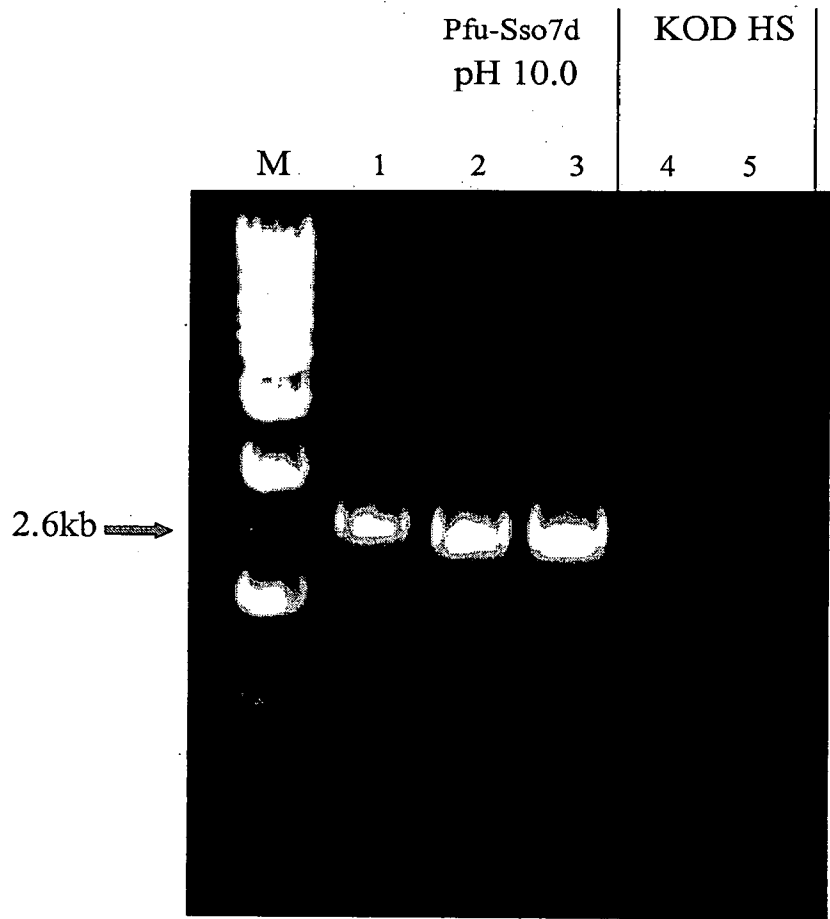
FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAgATgAACCCACTATTAgAgAAAAg-3' (SEQ ID NO: 5)

V93E#2

5'-CTTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 6)

V93R#1

5'-gAACATCCCCAAgATAgACCCACTATTAgAgAAAAg-3' (SEQ ID NO: 7)

V93R#2

5'-CTTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 8)

V93N#1

5'-gAACATCCCCAAgATAACCCCACTATTAgAgAAAAg-3' (SEQ ID NO: 9)

V93N#2

5'-CTTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 10)

V93H#1

5'-gAACATCCCCAAgATCACCCCACTATTAgAgAAAAg-3' (SEQ ID NO: 11)

V93H#2

5'-CTTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAgATNNKCCCACTATTAgAgAAAAg-3' (SEQ ID NO: 13)

FIGURE 10 (CONT.)

V93K#1

5'-gAACATCCCCAAgATAAACCCACTATTAgAg-3' (SEQ ID NO: 14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 15)

QCM#1   5'-(Phosphate)gAACATCCCCAAgATgCACCCACTATTAgAgAAAAg-(SEQ ID NO: 16)'

Alanine

QCM#2   5'-(Phosphate)gAACATCCCCAAgATgACCCCACTATTAgAgAAAAg-3'(SEQ ID NO: 17)

Aspartic Acid

QCM#3   5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAg-3' (SEQ ID NO: 18)

Cysteine

QCM#4   5'-(Phosphate)gAACATCCCCAAgATATACCCACTATTAgAgAAAAg-3' (SEQ ID NO: 19)

Isoleucine

QCM#5   5'-(Phosphate)gAACATCCCCAAgATATgCCCACTATTAgAgAAAAg-3' (SEQ ID NO: 20)

Methionine

QCM#6   5'-(Phosphate)gAACATCCCCAAgATTTCCCCACTATTAgAgAAAAg-3' (SEQ ID NO: 21)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCACTATTAgAgAAAAAg-3' (SEQ ID
NO: 22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID
NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACACCCACTATTAgAgAAAAAg- 3' (SEQ ID
NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID
NO: 25)

Tyrosine

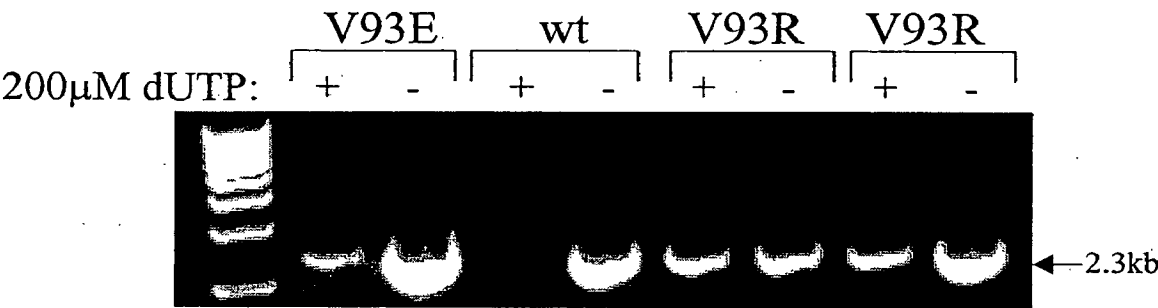**QCM#11** 5'-(Phosphate)gAACATCCCCAAgATTggCCCACTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

FIGURE 11

a.)

b.)
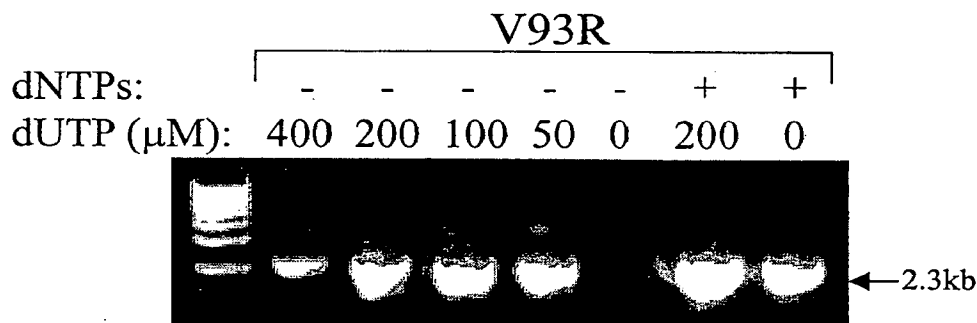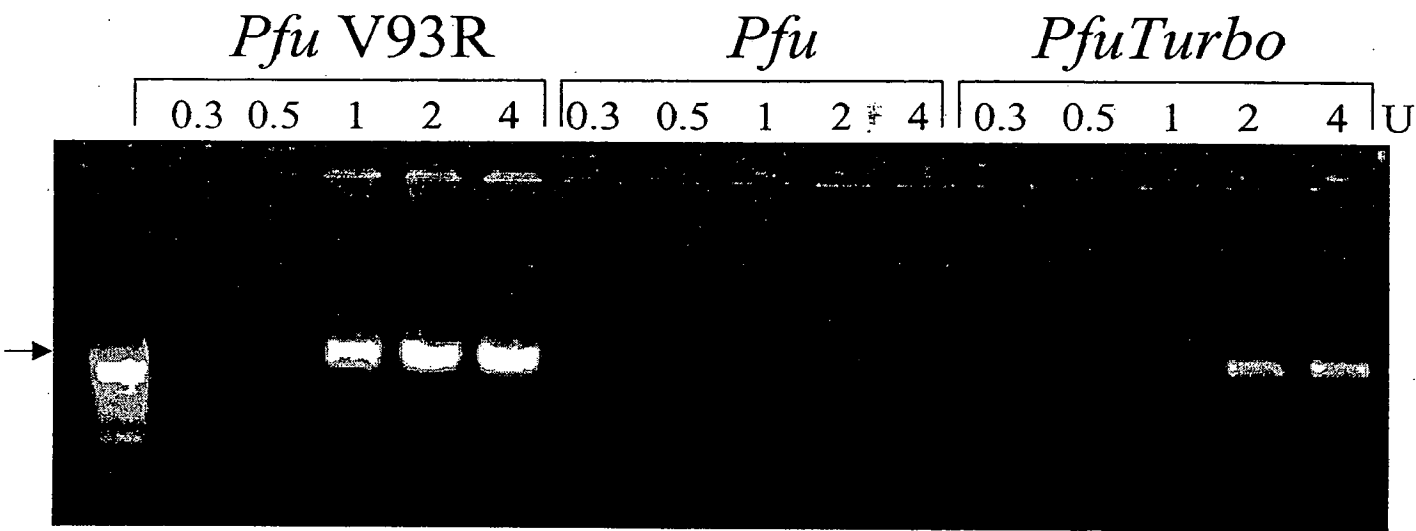
FIGURE 12

FIGURE 13A

PFU DNA POLYMERASE
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
28)

```
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AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
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GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
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GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
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PFU DNA POLYMERASE
G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 29)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
30)

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CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG AAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
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TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
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GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
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ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
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PFU DNA POLYMERASE
D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or
T)
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 31)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
32)

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AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
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ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATNNNC CCACTATTAG AGAAAAAGTT 300
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TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
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ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
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KOD DNA POLYMERASE
**V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 33)**
**V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
34)**

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CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
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AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
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Vent DNA POLYMERASE
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 35)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 36)

```
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GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
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GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
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Deep Vent
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 37)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO:
38)

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ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG   60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT  120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG  180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT  240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACNNNC CGCAATAAG GGATAAGATA  300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC  360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT  420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA  480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC  540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG  600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT  660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG  720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC  780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG  840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG  900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC  960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
.GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
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GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAGTAA                 2328
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JDF-3
V93R MUTANT: NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS
FOR ARGININE) (SEQ ID NO: 39)
V93E MUTANT: NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ ID NO: 40)

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ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCA
GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA
GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGGCAGGTCT
GTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACNNNCCGGCAATCCGCGACAAAATAAGGAAGCACCCCGCGG
TCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGA
GGAAGAGCTTAAACTCATGTCCTTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGATTCTG
ATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCT
CCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGG
CGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCTCGGGAGGGACGGGAGC
GAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCA
TAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGT
CTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCG
AGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGG
ACGTTTCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCC
CAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACgcCGGTGGCTACGTCAAGGAGCCGGAGCGGGGA
CTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCCTTCAATCATAATCACCCACAACGTCTCGCCAGATA
CGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTT
CATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTG
GAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCA
GGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGA
GCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCT
GAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTCGAACTCGAATACG
AGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCG
CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGG
CACGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGA
AGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAgcG
TTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGC
GACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTC
TGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGG
GCTTGGCGCGTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA
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>Pfu V93R (SEQ ID NO:41)
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A(SEQ ID NO:44)
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

FIGURE 13B (CONT.)

>Pfu V93E/G387P(SEQ ID NO:45)
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/D141A/E143A(SEQ ID NO:46)
MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT V93R(SEQ ID NO:47)
MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDRPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E(SEQ ID NO:48)
MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDEPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>TGO V93R(SEQ ID NO:49)

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDRPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E(SEQ ID NO:50)
MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R(SEQ ID NO:51)
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E(SEQ ID NO:52)
MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT V93R(SEQ ID NO:53)
MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E(SEQ ID NO:54)
MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R(SEQ ID NO:55)
MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSF[D]I[E]TLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLY[P]SIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK
ATLDPLEKNLLDYRQR[A]IKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E(SEQ ID NO:56)
MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR
SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSF[D]I[E]TLYHEGEEFGTGP
ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR
DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS
MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK
EPERGLWDNIVYLDFRSLY[P]SIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK
ATLDPLEKNLLDYRQR[A]IKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA
RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI
VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

Figure 14

Tgo 93:
NNN = AGA, AGG, CGA, CGC, CGG, CGT (R)
(NUCLEOTIDE SEQUENCE: SEQ ID NO: 57; AMINO ACID SEQUENCE: SEQ ID NO: 58)

NNN = GAA, GAG (E)
(NUCLEOTIDE SEQUENCE: SEQ ID NO: 59; AMINO ACID SEQUENCE: SEQ ID NO: 60)

```
5'
atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc      48
Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile
1               5                   10                  15

agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga      96
Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg
                20                  25                  30

aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att     144
Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile
            35                  40                  45

gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg     192
Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg
        50                  55                  60

gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata     240
Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile
65                  70                  75                  80

gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc     288
Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile
                85                  90                  95

agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac     336
Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr
                100                 105                 110

gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg     384
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
            115                 120                 125

atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg     432
Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr
        130                 135                 140

ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata     480
Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile
145                 150                 155                 160

agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc     528
Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile
                165                 170                 175

gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag     576
Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys
                180                 185                 190
```

FIGURE 14 (CONT.)

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cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc          624
Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr
        195             200             205

tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag          672
Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu
        210             215             220

aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa          720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys
225             230             235             240

atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att          768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act          816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
            260             265             270

tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag          864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu
            275             280             285

aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga          912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly
        290             295             300

tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat          960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr
305             310             315             320

gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc         1008
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
            325             330             335

gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc         1056
Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca         1104
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
            355             360             365

cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac         1152
Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr
        370             375             380

gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc         1200
Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile
385             390             395             400

gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat         1248
Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
            405             410             415

aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac         1296
```

FIGURE 14 (CONT.)

```
Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Glu Glu Tyr Asp
            420             425             430

gtg gct cct cag gta ggc cat aag ttc tgc aag gac ttc ccc ggc ttc     1344
Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe
            435             440             445

atc cca agc ctc ctc gga gac ctc ttg gag gag aga cag aag gta aag     1392
Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Val Lys
            450             455             460

aag aag atg aag gcc act ata gac cca atc gag aag aaa ctc ctc gat     1440
Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys Leu Leu Asp
465             470             475             480

tac agg caa cga gca atc aaa atc ctt gct aat agc ttc tac ggt tac     1488
Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr
                485             490             495

tac ggc tat gca aag gcc cgc tgg tac tgc aag gag tgc gcc gag agc     1536
Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser
                500             505             510

gtt acc gct tgg ggc agg cag tac atc gag acc acg ata agg gaa ata     1584
Val Thr Ala Trp Gly Arg Gln Tyr Ile Glu Thr Thr Ile Arg Glu Ile
                515             520             525

gag gag aaa ttt ggc ttt aaa gtc ctc tac gcg gac aca gat gga ttt     1632
Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Phe
            530             535             540

ttc gca aca ata cct gga gcg gac gcc gaa acc gtc aaa aag aag gca     1680
Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala
545             550             555             560

aag gag ttc ctg gac tac atc aac gcc aaa ctg ccc ggc ctg ctc gaa     1728
Lys Glu Phe Leu Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu
                565             570             575

ctc gaa tac gag ggc ttc tac aag cgc ggc ttc ttc gtg acg aag aag     1776
Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys
                580             585             590

aag tac gcg gtt ata gac gag gag gac aag ata acg acg cgc ggg ctt     1824
Lys Tyr Ala Val Ile Asp Glu Glu Asp Lys Ile Thr Thr Arg Gly Leu
                595             600             605

gaa ata gtt agg cgt gac tgg agc gag ata gcg aag gag acg cag gcg     1872
Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala
            610             615             620

agg gtt ctt gag gcg ata cta aag cac ggt gac gtt gaa gaa gcg gta     1920
Arg Val Leu Glu Ala Ile Leu Lys His Gly Asp Val Glu Glu Ala Val
625             630             635             640

agg att gtc aaa gag gtt acg gag aag ctg agc aag tac gag gtt cca     1968
Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro
```

FIGURE 14 (CONT.)

<pre>
               645   650   655

ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac   2016
Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp
            660   665   670

tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca   2064
Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala
            675   680   685

agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc   2112
Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu
            690   695   700

aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt   2160
Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe
705   710   715   720

gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag   2208
Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln
            725   730   735

gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa   2256
Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys
            740   745   750

gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg   2304
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
            755   760   765

cta aaa cct aag aca tga   2322
Leu Lys Pro Lys Thr
</pre>

FIGURE 15A
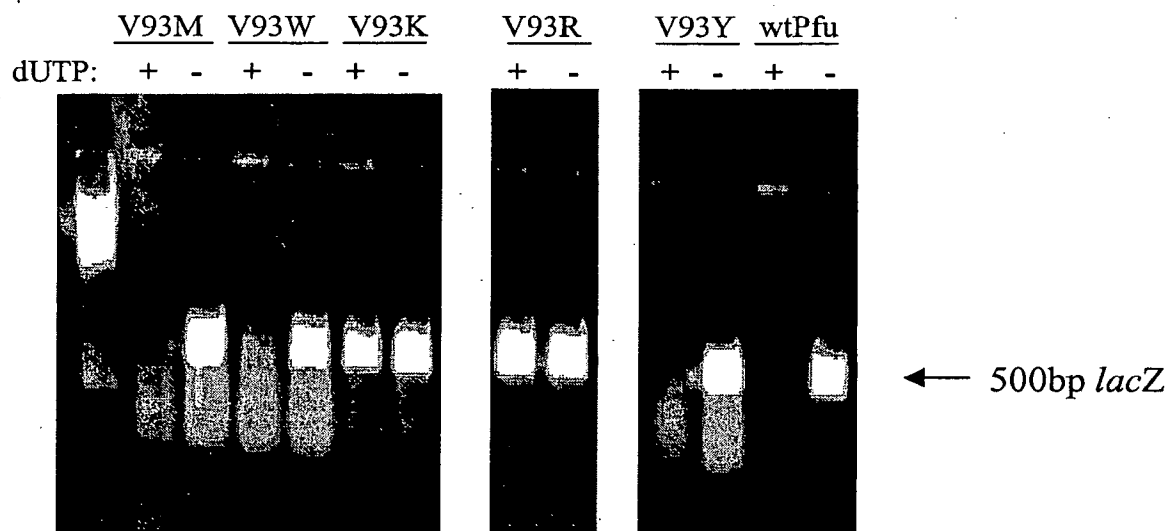
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

FIGURE 15B
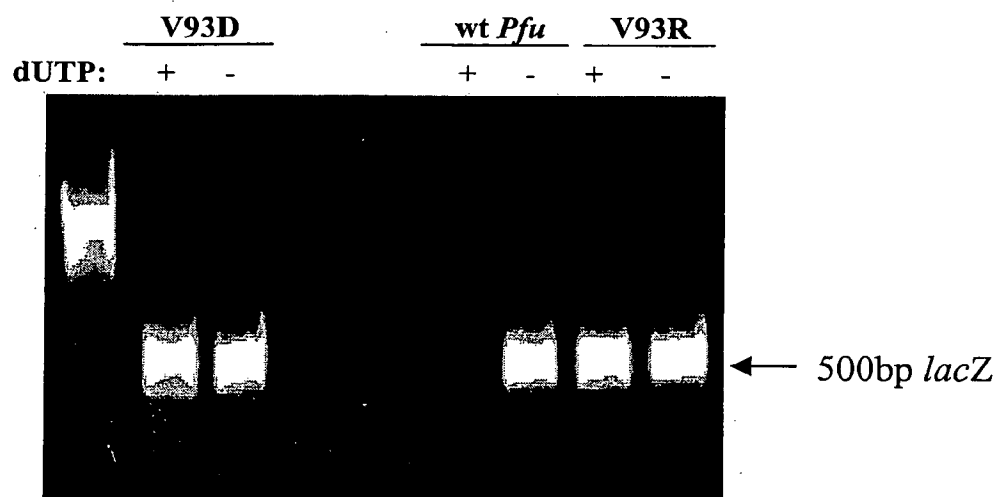
Results: The *Pfu* V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*.

FIGURE 15C
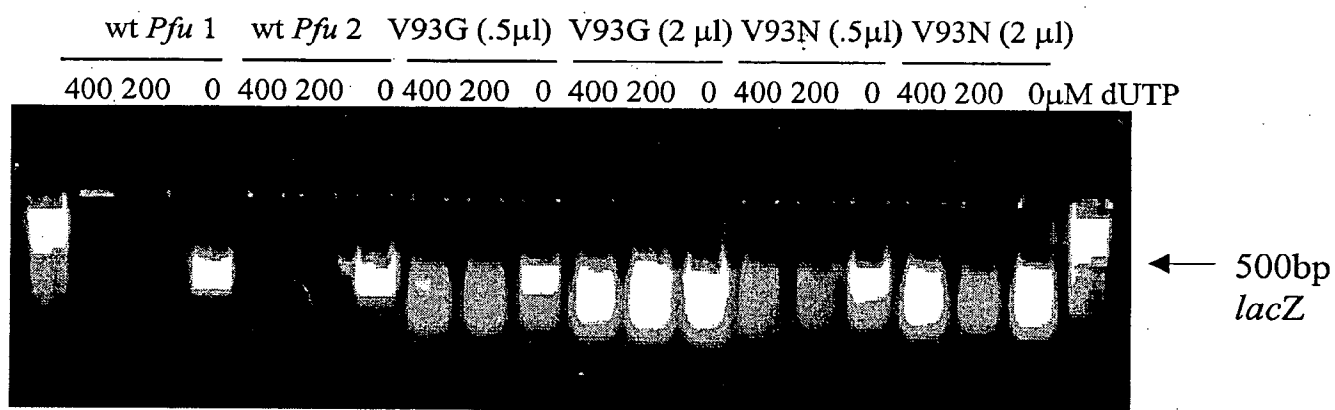
Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 16:   Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65°

Figure 17A

Pyrococcus furiosus gene for archaeal histone (HMf-like)
(ACCESSION No: AB013081)
Nucleotide sequence (SEQ ID NO: 63)
Amino acid sequence (SEQ ID NO: 64)

```
  M   M   G   E   L   P   I   A   P   V   D   R   L   I   R   K   A   G     18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54

  A   Q   R   V   S   E   Q   A   A   K   V   L   A   E   H   L   E   E     36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108

  K   A   I   E   I   A   K   K   A   V   D   L   A   K   H   A   G   R     54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA CAC GCA GGT AGA      162

  K   T   V   K   V   E   D   I   K   L   A   I   K   S   *               69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA             207
```

Figure 17B

(HMf-like)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65)
Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

```
  M   M   G   E   L   P   I   A   P   V   D   R   L   I   R   K   A   G     18
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54

  A   Q   R   V   S   E   Q   A   A   K   V   L   A   E   H   L   E   E     36
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108

  K   A   I   E   I   A   K   K   A   V   D   L   A   K   H   A   G   R     54
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA CAC GCA GGT AGA      162

  K   T   V   K   V   E   D   I   K   L   A   I   K   S                   69
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC
```

FIGURE 17B (CONT.)

```
     G   G   G
//  GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

 D   G   H   L   A   Y   R   T   F   F   H   A   L   K   G   L   T   T
GAC GGC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG TTT GAC AAG GCC GCC CCC

 S   F   R   H   E   A   Y   G   G   Y   K   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GGC CGG GCC CCC ACG CCA

 E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

 L   A   R   L   E   V   P   G   Y   P   Y   E   A   D   D   V   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC CCG TAC GAG GCG GAC GAC GTC GCC AGC CTG

 A   K   A   K   A   E   K   A   E   G   Y   E   V   R   I   T   A   D   K
GCC AAG GCG AAG GCG GAA AAG GCC GAG GGC TAC GAG GTC CGC ATC ACC GCC GAC AAA

 D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

 L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   P   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

 A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

 G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA
```

FIGURE 17B (CONT.)

```
A   L   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   R   E   P   D   E   R   L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC GAG AGG CTT

R   A   F   L   E   R   L   E   F   G   S   L   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT

L   E   S   P   K   A   L   E   E   A   P   W   P   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCC TGG CCC CCG GAA GGG GCC

F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG CCC ATG TGG GCC GAT CTT GCC

L   A   A   R   G   G   R   V   H   R   A   P   E   P   Y   K   A
CTG GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L   R   D   K   E   A   R   G   L   L   A   K   D   L   S   V   L
CTC AGG GAC AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A   E   G   R   E   G   L   P   P   G   D   D   P   M   L   L   A
GCC GAA GGC AGG GAG GGC CTT CCG CCC GGC GAC GAC CCC ATG CTC CTC GCC

Y   L   D   P   S   N   T   P   E   T   V   A   R   R   Y   G
TAC CTC GAC CCT TCC AAC ACC CCC GAG ACC GTG GCC CGG CGC TAC GGC

G   E   W   T   E   E   A   G   E   R   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC CTT TCC GAG AGG CTC TTC

A   N   L   W   G   L   E   G   E   E   R   L   W   L   Y   R
GCC AAC CTG TGG GGG CTT GAG GGG GAG GAG AGG CTC TGG CTT TAC CGG

E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   I
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG ATC
```

FIGURE 17B (CONT.)

```
A   R   L   E   A   E   V   F   R   L   A   G   H   P   F   N   L   N
GCC CGC CTC GAG GCC GAG GTC TTC CGC CTG GCC GGC CAC CCC TTC AAC CTC AAC

S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC

G   K   T   E   K   T   G   K   R   S   A   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC AGC GCC GCC GTC CTG GAG GCC

L   R   E   A   H   P   I   V   E   K   I   L   Q   L   Y   R   E   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG CTC TAC AGG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G   R   L   H   T   R   F   N   Q   T   A   T   G   R   L   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S   D   P   N   L   Q   N   A   E   G   L   P   L   G   R
AGC GAT CCC AAC CTC CAG AAC GCC GAG GGG CTT CCG CTT GGG AGG

I   R   A   F   I   A   E   E   G   H   L   V   A   L   D   N   R   Y
ATC CGC GCC TTC ATC GCC GAG GAG GGG CAC CTC GTG GCC GGC GAC AAC CGC TAT

S   Q   I   L   R   V   L   R   D   I   H   T   E   T   A   S   W   M   I
AGC CAG ATA CTC AGG GTC CTG CGC GAC ATC CAC ACC GAG ACC GCC AGC TGG ATG ATC

R   V   F   Q   E   G   G   R   M   L   P   R   A   R   L   S   Q   L   I
CGG GTC TTC CAG GAG GGG CGG ATG CTG ATG CCC CGC GCG CGG CTC TCC CAG CTG ATC

G   V   P   R   E   A   V   D   P   G   Y   L   G   E   L   A   M   F
GGC GTC CCC CGG GAG GCC GTG GAC CCC GGC TAC CTC GGC GAG CTA GCC ATG TTC

N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   I
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTG ATC

I   P   Y   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P   A
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC GCC

K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   G   Y
```

FIGURE 17B (CONT.)

```
          AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG GGC AGG CGG GGG TAC

           V   E   T   L   F   G   R   R   Y   V   P   D   L   E   A   R   V
          GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

           K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   Q   G
          AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

           T   A   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
          ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

           E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
          GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

           P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
          CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

           V   Y   P   L   A   V   P   L   E   V   G   I   G   E   D   W
          GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

           L   S   A   K   E   G   I   D   G   R   G   G   H   H   H
          CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT CAT

           H   H   *
          CAT CAT TAA
```

Figure 17C

Taq DNA polymerase- (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 64)

```
 G   G   G
GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG
```

FIGURE 17C (CONT.)

```
D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   V   G   Y   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC GGC TAC TTC GCC AAG AGC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GAC GGG GAC GCG GTG ATC GTG TTT GAC GCC AAG GCC CCC

S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   V   D   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG GTG GAC CTC CTG GGG

L   A   R   L   E   V   P   G   Y   E   A   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC GCC CTG AGC CTG

A   K   A   E   K   E   G   Y   E   V   R   I   T   A   D   K
GCC AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC ACC GCC GAC AAA

D   L   Y   Q   L   L   S   D   R   I   H   V   L   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC GAG GGG TAC

L   I   T   P   A   W   L   E   G   D   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT GAA ACC GGG GAC CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   A   R   K   L   N   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GCG AGG AAG CTT CCC GGG GTC AAG

G   I   G   E   K   T   L   E   S   D   L   L   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG CTG GAG TCC GAC CTT CTG GAG TGG GGG AGC CTG GAA

A   L   L   K   N   L   R   K   P   A   I   R   E   K   I   L
GCC CTC CTC AAG AAC CTG CGG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
```

FIGURE 17C (CONT.)

```
      L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
      CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

  R   A   F   L   E   R   L   E   F   G   S   L   H   E   F   G   L
  AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT

  L   E   S   P   K   A   L   E   E   W   P   P   P   E   G   A
  CTG GAA AGC CCC AAG GCC CTG GAG GAG TGG CCC CCG CCG GAA GGG GCC

  F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   A
  TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG ATG TGG GCC GAT CTT GCC

  L   A   A   R   G   G   R   V   H   R   A   P   E   P   Y   K   A
  CTG GCC GCC AGG GGG GGC CGG GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

  L   R   D   L   K   E   A   G   L   L   A   K   D   L   S   V   L
  CTC AGG GAC CTG AAG GAG GCG CGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

  A   L   R   E   G   L   G   L   P   P   G   D   P   M   L   A
  GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GGC GAC CCC ATG CTC GCC

  Y   L   D   P   S   N   T   T   P   E   G   V   A   R   Y   G
  TAC CTC GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG TAC GGC

  G   E   W   T   E   E   A   G   E   R   A   L   S   E   R   L   F
  GGG GAG TGG ACG GAG GAG GCG GGG GAG CGG GCC GCC CTT TCC AGG CTC TTC

  A   N   L   W   G   R   L   E   G   L   E   R   L   L   W   L   Y   R
  GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG CTC CTT TGG CTT TAC CGG

  E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
  GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

  R   L   D   V   A   Y   L   R   A   L   S   L   E   V   A   E   E   I
  CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CTG GAG GTG GCC GAG GAG ATC

  A   R   L   E   A   E   V   F   R   L   A   G   H   P   F   N   L   N
  GCC CGC CTC GAG GCC GCC GAG GTC TTC CGC CTG GCC GGC CAC TTC AAC CTC AAC

  S   R   D   Q   L   E   R   V   L   F   D   E   L   G   L   P   A   I
  TCC CGG GAC CAG CTG GAA AGG GTC CTC TTT GAC GAG CTA GGG CTT CCC GCC ATC
```

FIGURE 17C (CONT.)

```
G   K   T   E   K   T   G   K   R   S   T   S   A   A   V   L   E   A
GGC AAG ACG GAG AAG ACC GGC AAG CGC TCC ACC AGC GCC GCC GTC CTG GAG GCC

L   R   E   A   H   P   I   V   E   K   I   L   Q   Y   R   E   L   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG CAG TAC CGG GAG CTC ACC

K   L   K   S   T   Y   I   D   P   L   P   D   L   I   H   P   R   T
AAG CTG AAG AGC ACC TAC ATT GAC CCC TTG CCG GAC CTC ATC CAC CCC AGG ACG

G   R   L   H   T   R   F   N   Q   T   A   T   G   R   L   S
GGC CGC CTC CAC ACC CGC TTC AAC CAG ACG GCC ACG GGC AGG CTA AGT

S   D   P   N   L   Q   N   I   P   V   R   T   P   L   G   Q   R
AGC GAT CCC AAC CTC CAG AAC ATC CCC GTC CGC ACC CCG GGC CAG AGG

I   R   A   F   I   A   E   E   W   G   L   L   V   A   L   D   Y
ATC CGC GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S   Q   I   E   L   R   V   H   A   H   L   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC CTC TCC GGC GAC GAG AAC CTG ATC

R   V   F   Q   E   G   R   D   I   H   T   E   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

G   V   P   R   E   A   V   D   P   L   M   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG GCC GCG AAG ACC ATC

N   F   G   V   L   Y   M   G   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC ATG GGC TCG GCC CAC CGC CTC CAG GAG CTA GCC

I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC CGC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   R   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG CGG AGG CGG GGG TAC

V   E   T   L   F   G   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   A   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCC GCG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC
```

FIGURE 17C (CONT.)

```
T   A   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E   M   G   A   R   M   L   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   G   G   H   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGC GGA GGG CAT CAT CAT CAT

H   H   //
CAT CAT //
```

18
54

```
M   M   G   E   L   P   I   A   P   V   D   R   L   I   R   K   A   G
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT
```

36
108

```
A   Q   R   V   S   E   Q   A   A   K   V   L   A   E   H   L   E   E
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA
```

54
162

```
K   A   I   E   I   A   K   K   A   V   D   L   A   K   H   A   G   R
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA

K   T   V   K   V   E   D   I   K   L   A   I   K   S   *
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

69

Figure 17D

Pfu DNA Polymerase (WT) -(HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 61)   //Nucleotide sequence (SEQ ID NO: 63)

FIGURE 17D (CONT.)

//

cctggtcct gggtccacat atatgttctt actcgcctt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat

caactctaca cctccctat ttctctct atgagattt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtggggagc ataatgatt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc

aaagattgaa gaagttaaga aataacgggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta

tttggaacat ccccagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

aataccaatg gaggggaag aagagctaaa gattcctgcc ttcgatatag aaaccctcta

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat

agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact

tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag

gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga

gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

FIGURE 17D (CONT.)

```
ccttccaatg gaaattcagc ttccaagatt agttggacaa cctttatggg atgttccaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtccctcac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag aatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
```

FIGURE 17D (CONT.)

```
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct

aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttattta

tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct

cagagaattg agaaacatca gaaacttTga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct

acaattttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg //

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA    108
AAA GCT ATT GAG GTC GCA AAA AAG GCA GTA GAT CTT GCA AAG GCA CAC GCA GGT AGA    162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

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Figure 17E

(HMf-like) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 63)   //Nucleotide sequence (SEQ ID NO: 61)

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT GAG AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CTT GAG GAA   108
AAA GCT ATT GAG GTC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //
```

cctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa ctttagacc atacatttac gctccttctca gggatgattc

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aaggttgaga aaagtttct cggcaagcct attaccgtgt ggaaactta

tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

aataccaatg gaggggggag aagagctaaa gattcttgcc ttcgatatag aaaccctcta

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
```

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FIGURE 17E (CONT.)

```
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct
acaatttttt cctgtatctt cctaatgtat aagcaagcca aaggagagta gatgctacct
ttccgggagt tttgtattgc tctagccaag gttgggattt tttgaatcct ttaactctgg
aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt
taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta
```

FIGURE 17E (CONT.)

```
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat

agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact

tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca aggaagaat  acattcgac  ttgtatcatg taataacaag

gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga

gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag

gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga

agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt

tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat

ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac

aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactact gacaaaaagc

gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg

gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta

tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag

gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
```

FIGURE 17E (CONT.)

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtccctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg // TGA

Figure 17F

(HMf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63)   // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 63)   // Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT       54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CTT GAG GAA             108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA        162
AAG ACC GTT AAG GTC GAA GAC GTC GCA ATT AAG CTC GCA ATT AAG AGC //
```

```
//ATGGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
```

REPLACEMENT SHEET

FIGURE 17F (CONT.)

```
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAAATTGCA 1860
AAAGAAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATAAGGCGAT ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCCAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAAG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
// TGA
```

Figure 17G

__PFU DNA POLYMERASE (V93 __R OR E__) - (HMf-like) fusion protein__

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 63)

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FIGURE 17G (CONT.)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA    60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT   120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA   180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT   240
ACCGTGTGGA AACTTTATTT GGAACATCCC CCACTATTAG AGAAAAAGTT AGAAAAAGTT   300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG   660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG   780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGAA  ATTCAGCTTT CAAGATTAGT TGGACAACCT  1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA  1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG  1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC  1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT  1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC  1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA  1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT  1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT  1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG  1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT  1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAGAAAAAAG  1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AGCTCCCTGA GACTGCTAGA GCTTGAAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA  1800
GAAGGAAAAG TCATTACTCG ATAGTTAGGA ACGGAGATGT GAGATTGGAG TGAAATTGCA  1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT  1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG  1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC  2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT  2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA  2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA  2220
```

```
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //          2328
```

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA AAG GTA CTT GCA GAG CTT GCA GAG GAA       108
AAA GCT ATT GAG GTC GCA AAA AAG GCA GTA GAT CTT GCA GTA GCA GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) -(HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT   120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA   180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT   240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT   300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAT TTCTCAGGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCCATTCCC ATATTTAGCG   660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG   780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT   1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA   1080
GCCTACGAAA GAAACGAAGT AGCTCCCAAAC AGCTCCAAGT AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG   1140
```

```
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTCGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //               2328
```

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

Figure 17I

(HMf-like)-PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
```

FIGURE 17I (CONT.)

```
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //


//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT   120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA   180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT   240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT   300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG   660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG   780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT   1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA   1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG   1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC   1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT   1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC   1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA   1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT   1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT   1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG   1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT   1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG   1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT   1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA   1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA   1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT   1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG   1980
CTCGCCAATAT ATGAGACAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTTCCTCAC   2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT   2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA   2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA   2220
```

GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG   2328

Figure 17J

(HMF-LIKE)-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTTCTCAGG GATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAAATA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020

FIGURE 17J (CONT.)

```
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACCA GGT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //             2328
```

TGA

Figure 17K

PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (HMF-LIKE) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA  60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATGTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAGAAA AGTTTCTCGG CAAGCCTATT 240
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FIGURE 17K (CONT.)

```
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT  300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC  360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC  420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT  480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC  540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG  600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG  660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GGTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT TTCCATTAAA AATCC //         2328
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ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA  108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG GCA GCA GGT AGA  162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

Figure 17L

KOD DNA POLYMERASE - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 33)   // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 34)   // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG   60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC  120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG  180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT  240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA  300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC  360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC  420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA  480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC  540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG  600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA  660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG  720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC  780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA  840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA  900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC  960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAAGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGCCAC  AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
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FIGURE 17L (CONT.)

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ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCCGAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTAAGG CCGAAGGGAA CT 2325
//

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA    108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA    162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

Figure 17M

(HMf-like) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA    108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA    162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ATGATCCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG    60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC   120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG   180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT   240
GAGGTCTCGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA   300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC   360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC   420
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```
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGCCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325
```

Figure 17N

(HMf-like)-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

FIGURE 17N. (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) ;

```
ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT               54
GCT CAG AGA GTT GAG AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA      108
AAA GCT ATT GAG GTC GCA ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA  162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG GAC AGC //
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```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG    60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT   120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA   180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT   240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGAC̲X̲X̲X̲C CAGCTATGCG GGGCAAAATA   300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT   360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT   420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT   480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT   540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA   600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA   660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA   720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT   780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT   840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA   900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA   960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT  1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA  1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA  1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG  1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC  1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA  1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT  1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA  1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG  1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG  1560
AGACACTACA TAGAGATGAA GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT  1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA  1680
AAGAAAGCCA AGGAATTCCT AAACTACACA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT  1740
GAGTATGAGG GCTTTTACTT GAGAGAGATTC TTTGTTACAA AAAAGGCGCTA TGCAGTCATA  1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG  1860
```

FIGURE 17N (CONT.)

```
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GCAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
```

Figure 17O

Vent DNA POLYMERASE - (HMf-like) FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35)   // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 36)   // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGAA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC TACCCTTTGC CAAGCGTTAT CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AAAATATCGA AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGA AAAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAG AGGTTTGTGG 1200
```

```
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGAGAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GCAGATTACC AGGGATTTAA CAAAATACAG 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AAGACTTGCC GCAAGAGGGA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AGACTTGTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
```

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA CTT GCA CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA     162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

Figure 17P

Deep Vent- (HMf-like) DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG     60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT    120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG    180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAAG AGTTCCTGGG GAGGCCGATT    240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA    300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC    360
```

FIGURE 17P (CONT.)

```
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGAA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCTGGGAA  GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC   780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC   960
GAGCTCGGTA GGGAGTTCTT CCCAGCTTT  GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC  1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AAGCCGGATG AGTGGTACCT CCTCAGGAAG  1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG  1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAAGGGCT CTGGGAGGGG  1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA  1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC  1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT  1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC  1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA  1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA  1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA  1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC  1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG  1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC  1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA  1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG  1980
CTAGTTATTT ACGAGACAGAT CACGAGCGCC CTTCACGAGT ACAAGGCTAT AGTCCGCAC   2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA  2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG  2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT  2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG  2280
ACTAAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG //             2328
```

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

FIGURE 17Q

(HMflike) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 37)
Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT    54
GCT CAG AGA GTT AGC GAG GTT CAA GCA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA   108
AAA GCT ATT GAG GTC GCA ATC AAG AAG GTA GAT CTT GCA GAT CAC CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA
```

```
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAGAAAACG  GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG AGTTCCTGGG GAGGCCGATT   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA   300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360
CTAATAGACA AAGGCCTAAT TCCAATGAA  GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGAA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC   780
TACCACGTGA TTAGAGAAC  GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC   960
GAGCTCGGTA GGGGAGTTCT TCCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC  1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG  1080
GCCTACGAGA GGAATGAATT GGCTCCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG  1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG  1200
TTAGTTTCCC TAGATTTCAG GAGCCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA  1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC  1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT  1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC  1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA  1560
```

FIGURE 17Q (CONT.)

```
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA   1620
GACACAGATG GACTCCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA   1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGTCCCAG GGCTGTTGGA GCTTGAGTAC   1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG   1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC   1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA   1920
GTAAAGATAG TTAAGGAGGT CTGAGCAAGT ACGAAATACC TCCAGAAAAG   1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC   2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA   2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT   2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAACAGA CAGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA                 2328
```

Figure 17R

JDF-3 - (HMf-like) fusion protein

Nucleotide sequence (SEQ ID NO: 39)   // Nucleotide sequence (SEQ ID NO: 63)
Nucleotide sequence (SEQ ID NO: 40)   // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAGGTGAAGCCGAGTTCGAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGGCCTCCTCAGGAGACGACTCTGCCATCGAAGAATCAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAAGGTGAAGAAAAGTTCCTCGG
CAGGTCGTGTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGACAAAATAAGGAGCAATCTCGACATCTACGAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTTAATCCCGATGGAAGTGAGGAGAGCTTAAACTCATGTCTTCTCGAGATCGAGACGCTCTACCAGGGAGAAGAGTTTGAA
CCGGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGTGATAACTGGAAGAAGATCGAACTTCCTTACGTTGAGTTGTCTCCACCGAGAAGGAGATGATTAA
GCGCTTCTTGAGGGTCGTTAAGGAGGAAGAGGACGGGCCGAAGTGCTGATAACATACAACAGGTTTGCGTGGAAGCGTGTGAGAAGCTTGGCGTGAGCTTT
ACCCTCGGGAGGGAGGCGGAGCGGAGCCGAAGTACAGCGCATGGGGACAGGTTTCGGCAAGCCCAAGGAGAGAAGGTTCTTCCGATGGAGCGTTGGACGTTTCC
ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGCGAGGTTACTACGAGGTTACCTAAGGAGGTTCCTCCTCAAGAAGCAACTCGCTGCTGGAGAGGGGGGCT
GGTGGCGCGCTACTCGATGGAGGACGCGAGTGGTTGTTCCTCCTCAAGAAGCAACTCGTTCGTAGTCTCTAGACTTTCGTAGTCTCTACTATATCACACCGCCAGATAC
CGCTCAACGGCACCGGCAACCTCGTCGAGCGAGGTTGCCCCGAGTGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGCGTTCATTCGACCGAGTCCGGAAAGG
ACgCCGGTGGCTACGTCAAGAGCCGGAGCGCGGAGTACGACGTTGCCGAGGTGGGAGGAGCGTTACGGCGTTGATTCAGCGCGGCATGGTCATCGAAATGTCATCAGAGAACAGTGGAAATGGGGAAGGAGTACATCGAAGAAAGGCAATGGAGTTCTTAAACTATATCAATCCGGCCTTCTC
CTATGCAGAACAGACAGCGTCTCCATGCCACCATTCCTGGAGCGGACGCGTCAAGAAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCGGCCTTCTC
CAGAAGATAAAGAGAGGAAGATGAAAGCAACTCTCCTCGATTACAGCAACGCGCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCAAGGAGTACATCGAAATGTCATCAGAGACTTGAGGAAATGTCATCAGAGACTAC
GAACTCGAATACGAGGGCTTCTACGTGACGTCAGGGGGCTTCTGCTTCTCGCTGGGGCTTCTTCGTCGTCTCACGCGCGGCGGCTTGAGATAGTCAGGCGCG
```

ACTGGAGCGAGATAGCGAAGGAGGAACGCGAGGCGGAGGGTTTGGAGGCGGATCGGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGAGAGTCACCGGGAAAAGCTGAGCAA
GTACGAGGTTCCGCGGAGAGACTGGTTATCCACGAGCAGATAACGCGGAGCTCAAGGACTACAAGCCACCGGCCCGACCGGCCATAGCGAAGCGTTGGCCGCCAGAGGT
GTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGGATTCCCTTCGACGAGTTCGACGAGCACAAGTACGATG
CGGACTACTACATCGAGAACCAGGTTCTGCGCGGCAGTTCTGCGGCAGTTGAGAGAATCCTCGGGCTACCGGCAGGAAGACCTGCGCTGCGCGAAGAGACGAGGCCTTGGCGC
GTGGGCTGAAGCCGAAGGGGAAGAAGAAG//

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC AGC CAA GCA GCA CTT GCA CTT GCA CTT GCA CAC CAC GCA GGT GAA   108
AAA GCT ATT GAG GCT GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17S

__(HMf-like) - JDF-3 fusion protein__

Nucleotide sequence (SEQ ID NO: 63)   // Nucleotide sequence (SEQ ID NO: 39)
Nucleotide sequence (SEQ ID NO: 63)   // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT   54
GCT CAG AGA GTT AGC AGC CAA GCA GCA CTT GCA CTT GCA CTT GCA CAC CAC GCA GGT GAA   108
AAA GCT ATT GAG GCT GCA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA   162
AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

ATGATCCTTGACGTTGATTACATCACCGAGAATGAAAGCCCGTCATCAGGGTCTTCAAGAGAAGGAGAACGGCGGAGTTCGAGGATTGAATACGACCGGCGAGTTCGAGCC
CTACTTCTACGCGCTCCTCAGGGACGACTCTGGAGTTCTGTGGAGTCGCCATCGAGAAAATCAAAAAGATAACCGCGGAGAGAGATAACCGGGAGAGGAGGTCGTTAAGGTTAAGCGCGGAGAAGGTGA
AGAAAAAGTTCCTCGGCCAGGTACGACATACCCTCGTGGTCTGGAGTCCAAGCGCAATCCGCAGCAGACXXXCCGGCAATCCGCAGGAGTTAAGGAAGAATAAGGAGAAGCACCCGCGGTCATC
GACATCTACGAGTACGACATACCCTCGCCAAGCGCTAATCCGATGGAAGCTTAAACTCATGTCCTTCGACATCGA
GACGCTCTACCACGAGGGAGAGAGAGTTGGAACGGGCCGATTCTGATGATAAGCTACGCCGATGAGAAAGCGAGGCGCGGTGATAACCTGGAAGAAGATCGGCGACAACTTC
CTTACGTTGAGGTTGTCTCCACCGAGGAAGAGATGATTAAGCGCTTCTTGAGGGGTCGTTAAGGAGGAAGACTCCCTCGGGAGGAGGAGCTTACCCTCCGGGAGGAGACGGGGACCAGGTTTGCGGT
GACTTCGCTACCTACTACTTGAGAAAAGCGTTGGCTGAGCTTTATCCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCGACCTTGAGCGGCTGATAAACGGCTGTATACGAGCGCGGTTTTCGGCAAGC
CCAAGGAGAAGGTACGCGAGGAGATAGCCACCGGCCTGGGAGGGCTTGAGAGGTCGCGCGCTACTGATGGAGGACGGGCGAGGGTTACCTACGAG
CTTGGCAGGAGAGTTCTTCCCGATGGAGGGGTCATCGGCCAAGGCCTCTGGGACGTTCCCGCTCCAGCCCAACCTCGTCGAGTCGAGTGGTTCCT
CCTAAGGAGAAGGCCTACGAGAGGAACGAACTCGCTCCCAACAAGCCGGGGGCTACGCCGGTGGCTACGTCAAGGAGCCGG
AGCGGGGACTGTGGACAATATCGTGTATCTGACACTTTCGTAGTCTTCAATCATAATCACCCACAAATCGCTCCGCAGATACGCTCAACCGCGAGGGGTGT
AGGAGCTACGACGTTGCCCCGGAGGTCGGTCACAAGTTCTGCAAGAGACTTCCCCGGGCTTCATTCCGAAAACCTGCTCGAGGACTTCCCCCGGGCTTCATTCCGAAAACCTGCTCGAGGAAGAAGGCAGAAGATAAA

FIGURE 17S (CONT.)

GAGGAAGAGATGAAGGCAACTCTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCATCAAGAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG
CCAGGGCAAGAGATGGTACTGCAGGGACTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAA
GTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCAAACT
GCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCG
GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCACGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAATT
GTCAGGGAAGTCACCGAAAAGCTGAGCAAGTCGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGGAAGCTACGAGCGCCGAGCTCAAGGACTACAAGGCCACCGGCCC
GCACGTAGCCATAGCGAAGcGTTTGGCCGCCGACGACAGCGTTGTTAAAATCCGGCCGCTACTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG
CGATTCCCTTCGACGAGTTCGACCCGACGACGCCGACTACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGC
TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGCGTTGGCGCGTGGCTGA

Figure 17T

Pyrococcus furiosus DSM 3638, Archeael hostone (HMf-1) section 85 of 173 of the complete genome.
ACCESSION No: AE010210 REGION: complement (8333..9082)
/product="pcna sliding clamp (proliferating-cell nuclear antigen)"

Nucleotide sequence (SEQ ID NO: 67)
Amino acid sequence (SEQ ID NO: 68)

```
M   P   F   E   I   V   F   E   G   A   K   E   F   A   Q   L   I   D         18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54

T   A   S   K   L   I   D   E   A   A   F   K   V   T   E   D   G   I         36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA     108

S   M   R   A   M   D   P   S   R   V   V   L   I   D   L   N   L   P         54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG     162

S   S   I   F   S   K   Y   E   V   E   P   E   T   I   G   V   N             72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GAA CCA GAA ACA ATT GGA GTT AAC         216

M   D   H   L   K   K   I   L   K   R   G   K   A   K   D   T   L   I         90
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA     270

L   K   G   E   E   N   F   L   E   I   T   I   Q   G   T   A   T            108
CTC AAG GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACT GCA ACA         324

R   T   F   R   V   P   L   I   D   V   E   E   M   E   V   D   L   P        126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA     378

E   L   P   F   T   A   K   V   V   L   G   E   V   L   K   D   A           144
GAA CTT CCA TTC ACT GCA AAG GTT GTA GGA GAA GTT CTT GGA GAA GTC CTA AAA GAT GCT   432

V   K   D   A   S   L   V   S   D   I   K   F   I   A   R   E   N           162
```

FIGURE 17T (CONT.)

```
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT   486

 E   F   I   M   K   A   E   G   E   T   Q   E   V   E   I   K   L   T   180
GAA TTT ATA ATG AAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540

 L   E   D   E   G   L   D   I   E   V   Q   E   T   K   S   A           198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG ACA AAG AGC GCA   594

 Y   G   V   S   Y   L   S   D   M   V   K   G   L   G   K   A   D   E   216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   648

 V   T   I   K   F   G   N   E   M   P   M   Q   M   E   Y   Y   I   R   234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA   702

 D   E   G   R   L   T   F   L   A   P   R   V   E   E   *             250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA         750
```

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65)
Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

```
 M   P   F   E   I   V   F   E   G   A   K   E   F   A   Q   L   I   D    18
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54

 T   A   S   K   L   I   D   E   A   A   F   K   V   T   E   D   G   I    36
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA  108

 S   M   R   A   M   D   P   S   R   V   L   I   D   L   N   L   P      54
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG  162
```

FIGURE 17U (CONT.)

```
S   S   I   F   S   K   Y   E   V   V   E   P   E   T   I   G   V   N      72
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216

M   D   H   L   K   K   I   L   R   G   K   A   K   D   T   L   I          90
ATG GAC CAC CTA AAG AAG ATC CTA AGA GGT AAA GCA AAG GAC ACC TTA ATA       270

L   K   G   E   E   N   F   L   E   I   T   Q   I   G   T   A   T          108
CTC AAG GGA GAG GAA AAC TTC TTA GAG ATT ACA CAA ATT GGA GCA ACA           324

R   T   F   R   V   P   L   I   D   V   E   M   E   V   D   L   P          126
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA ATG GAA GTT GAC CTC CCA       378

E   L   P   F   T   A   K   V   V   L   G   E   V   L   D   A              144
GAA CTT CCA TTC ACT GCA AAG GTT GTA CTT GGA GTC CTA GAT GCT               432

V   K   D   A   S   L   V   S   D   I   K   F   I   A   R   E   N          162
GTT AAA GAT GCC TCT CTA GTG AGT GAC ATA AAA TTT ATT GCC AGG GAA AAT       486

E   F   I   M   K   A   E   G   E   T   Q   E   V   E   I   K   L   T      180
GAA TTT ATA ATG AAG GCA GGA GAG GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540

L   E   D   E   G   L   L   D   I   E   V   Q   E   T   K   S   A          198
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA       594

Y   G   V   S   Y   L   S   D   M   V   K   G   L   A   K   D   E          216
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   648

V   T   I   K   F   G   N   E   M   P   Q   M   E   Y   Y   I   R          234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC CAA ATG GAG TAT TAC ATT AGA       702

D   E   G   R   L   T   F   L   A   P   R   V   E   E                     250
GAT GAA GGA AGA CTT ACA TTC CTA GCT CCA AGA GTT GAA GAG

G   G   G
// GGC GGC GGT

V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
```

FIGURE 17U (CONT.)

```
                GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

S   R   G   E   P   V   Q   A   Y   G   F   A   K   S   A   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG TAC GGC TTC GCC AAG AGC CTC CTC CTC AAG

A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG TTT GAC GCC AAG GCC GCC CCC

S   F   R   H   E   H   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG CAC GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

E   D   F   P   R   Q   L   A   L   I   K   E   A   D   D   V   D   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG GCG GAC GAC GTG GTG CTC GGG

L   A   R   L   E   V   P   G   Y   E   Y   R   I   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG TAC CGC ATC CTC GCC AGC CTG

A   K   A   K   E   A   E   G   Y   E   Y   V   I   T   A   D   K
GCC AAG GCG AAG GAA GCG GAG GGC TAC GAG TAC GTC CGC ATC ACC GCC GAC AAA

D   L   Y   Q   L   S   D   R   I   H   V   H   P   E   G   Y
GAC CTT TAC CAG CTC TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   T   G   D   E   S   D   N   L   P   P   V   K
GCC GAC TAC CGG GCC ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A   L   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
GCC CTC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG
```

FIGURE 17U (CONT.)

A GCC	H CAC	M ATG	D GAC	D GAT	L CTG	K AAG	L CTC	S TCC	W TGG	D GAC	L CTG	A GCC	K AAG	V GTG	R CGC	T ACC	D GAC
L CTG	P CCC	L CTG	E GAG	V GTG	D GAC	F TTC	A GCC	K AAA	R AGG	R CGG	E GAG	P CCC	D GAC	R CGG	E GAG	R AGG	L CTT
R AGG	A GCC	F TTT	L CTG	E GAG	R AGG	L CTT	E GAG	F TTT	E GAG	G GGC	S AGC	L CTC	H CAC	E GAG	F TTC	G GGC	L CTT
L CTG	E GAA	S AGC	P CCC	K AAG	A GCC	A GCC	L CTG	E GAG	E GAG	A GCC	W TGG	P CCC	P CCG	P CCG	E GAA	G GGG	A GCC
F TTC	V GTG	G GGC	F TTT	V GTG	L CTT	S TCC	R CGC	K AAG	E GAG	P CCC	M ATG	W TGG	A GCC	D GAT	L CTT	L CTG	A GCC
L CTG	A GCC	A GCC	R AGG	G GGG	A GCC	R CGG	V GTC	R CGG	H CAC	A GCC	P CCC	E GAG	P CCT	Y TAT	K AAA	A GCC	
L CTC	R AGG	D GAC	L CTG	K AAG	E GAG	G GGG	L CTT	R CGG	K AAA	A GCC	D GAC	K AAA	L CTG	S AGC	D GAC	V GTT	L CTG
A GCC	D GAC	L CTG	E GAG	G GGG	P CCC	L CTC	D GAC	P CCC	K AAA	D GAC	A GCC	L CTC	R CGG	R CGG	M ATG	L CTC	A GCC
Y TAC	L CTC	D GAC	P CCT	S TCC	N AAC	T ACC	T ACC	P CCC	E GAG	G GGG	V GTG	A GCC	R CGG	R CGC	R CGG	Y TAC	G GGC
G GGG	E GAG	W TGG	T ACG	E GAG	E GAG	A GCG	G GGG	E GAG	R CGG	A GCC	L CTT	A GCC	L CTT	S TCC	E GAG	R AGG	F TTC
A GCC	N AAC	L CTG	W TGG	G GGG	R AGG	L CTT	E GAG	G GGG	E GAG	E GAG	R AGG	L CTC	L CTT	W TGG	L CTT	L CTT	Y TAC	R CGG
E GAG	V GTG	E GAG	R AGG	P CCC	L CTT	S TCC	A GCT	V GTC	L CTG	A GCC	H CAC	M ATG	E GAG	A GCC	T ACG	G GGG	V GTG
R CGC	L CTG	D GAC	V GTG	A GCC	Y TAT	L CTC	R AGG	A GCC	L CTC	S TCC	L CTG	E GAG	V GTG	A GCC	E GAG	I ATC	

FIGURE 17U (CONT.)

```
A    R    L    E    A    E    V    F    R    L    A    G    H    P    F    N    L    N
GCC  CGC  CTC  GAG  GCC  GAG  GTC  TTC  CGC  CTG  GCC  GGC  CAC  CCC  TTC  AAC  CTC  AAC

S    R    D    Q    L    E    R    V    L    F    D    E    L    G    L    P    A    I
TCC  CGG  GAC  CAG  CTG  GAA  AGG  GTC  CTC  TTT  GAC  GAG  CTA  GGG  CTT  CCC  GCC  ATC

G    K    T    E    K    T    G    K    R    S    T    S    A    V    A    L    E    A
GGC  AAG  ACG  GAG  AAG  ACC  GGC  AAG  CGC  TCC  ACC  AGC  GCC  GTC  GCC  CTG  GAG  GCC

L    R    E    A    H    P    I    V    E    K    I    L    Q    Y    R    E    L    T
CTC  CGC  GAG  GCC  CAC  CCC  ATC  GTG  GAG  AAG  ATC  CTG  CAG  TAC  CGG  GAG  CTC  ACC

K    L    S    T    Y    I    D    F    N    L    P    D    I    H    P    R    T
AAG  CTG  AGC  ACC  TAC  ATT  GAC  TTC  AAC  CTG  CCG  GAC  ATC  CAC  CCC  AGG  ACG

G    R    L    H    T    N    Q    T    A    T    R    A    I    G    R    L    S
GGC  CGC  CTC  CAC  ACC  AAC  CAG  ACG  GCC  ACG  CGC  GCC  ATC  GGC  AGG  CTA  AGT

S    D    P    N    L    A    E    G    W    L    T    P    V    R    Q    R
TCC  GAT  CCC  AAC  CTC  GCC  GAG  GGG  TGG  CTA  ACG  CCG  GTC  CGC  CAG  AGG

I    R    A    F    I    A    E    E    W    L    V    A    L    D    Y
ATC  CGG  GCC  TTC  ATC  GCC  GAG  GAG  TGG  TTG  GTG  GCC  CTG  GAC  TAT

S    Q    I    E    L    R    L    R    V    L    A    H    S    D    E    N    L    I
AGC  CAG  ATA  GAG  CTC  AGG  CTC  AGG  GTG  CTA  GCC  CAC  TCC  GAC  GAG  AAC  CTG  ATC

R    V    F    Q    E    G    V    P    R    T    E    T    A    S    W    M    F
CGG  GTC  TTC  CAG  GAG  GGG  GTG  CCC  CGC  ACG  GAG  ACC  GCC  AGC  TGG  ATG  TTC

G    V    P    R    E    A    V    D    P    L    P    T    G    L    G    Q    R
GGC  GTC  CCC  CGG  GAG  GCC  GTG  GAC  CCC  CTG  CCG  ACC  GGG  CTT  GGG  CAG  AGG

N    F    G    V    L    Y    G    M    S    A    H    R    L    S    Q    E    L    A
AAC  TTC  GGG  GTC  CTC  TAC  ATG  TCG  GCC  CAC  CGC  CTC  TCC  CAG  GAG  CTA  GCC

I    P    Y    E    A    Q    A    F    I    E    R    Y    F    Q    S    F    P
```

FIGURE 17U (CONT.)

```
      ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

  K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   R   G   Y
  AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG CGG GGG TAC

  V   E   T   L   F   G   R   R   R   Y   V   P   D   L   E   A   R   V
  GTG GAG ACC CTC TTC GGC CGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

  K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   Q   G
  AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

  T   A   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
  ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

  E   M   G   A   R   M   L   Q   V   H   D   E   L   V   L   E   E   A
  GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

  P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
  CCA AAA GAG AGG GCG GAG GCG GAG GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

  V   Y   P   L   A   V   P   L   E   V   G   I   G   E   D   W
  GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GGG ATA GGG GAG GAG GAC TGG

  L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
  CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC CGC GGC GGA GGC GGG CAT CAT CAT

  H   H   *
  CAT CAT TAA
```

Figure 17V

Taq DNA polymerase- (PCNA) fusion protein

FIGURE 17V (CONT.)

Nucleotide sequence (SEQ ID NO: 65) /Nucleotide sequence (SEQ ID NO: 67)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68)

```
      G   G   G
   // GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

 D   G   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A   L   K   E   D   G   D   A   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG. GAC GCG GTG ATC GTG TTT GAC GCC AAG GCC CCC

 S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   T   P
TCC TTC CGC CAC GAG GCC TAC GGG GGG TAC AAG GCG GGC CGG GCC ACG CCA

 E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

 L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

 A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA GAG AAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA

 D   L   Y   Q   L   S   D   R   I   H   V   L   .H   P   E   G   Y
GAC CTT TAC CAG CTC TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

 L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG
```

FIGURE 17V (CONT.)

```
A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   E   L   E   W   G   S   L   E
GGG ATC GGG GAG AAG ACG GCG AGG AAG GAG CTT GAG TGG GGG AGC CTG GAA

A   L   K   N   L   D   R   L   P   A   I   R   E   K   I   L
GCC CTC AAG AAC CTG GAC CGG CGG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   K   L   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT AAG CTG TCC TGG GAC CTG GCC AAG GTG ACC GAC

L   P   L   E   V   D   F   A   K   R   R   D   P   R   E   R   L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAC CCC CGG GAG AGG CTT

R   A   F   L   E   R   L   E   F   G   S   L   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT

L   E   S   P   K   A   L   E   E   P   W   P   P   E   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC TGG CCC CCG GAA GAG GGG GCC

F   V   G   F   V   L   S   R   E   K   W   P   M   W   A   D   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG TGG CCC ATG TGG GCC GAT CTG GCC

L   A   A   R   G   G   R   V   H   R   A   P   E   P   Y   K   A
CTG GCC GCC GCC AGG GGG CGG GTC CAC CGG GCC GCC GAG CCT TAT AAA GCC

L   R   D   L   K   E   A   R   G   L   L   A   K   D   L   S   V   L
CTC AGG GAC GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC AGC GTT CTG

A   L   R   E   G   L   G   L   P   P   D   P   M   L   L   A
GCC CTG AGG GAA GGC CTT GGC CTC CCG CCC GAC GAC CCC ATG CTC CTC GCC

Y   L   D   P   S   N   T   T   P   E   G   V   A   R   L   G
TAC CTC CTG GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG TAC GGC

G   E   W   T   E   E   A   R   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GCG CGG GAG GCC CTT TCC GAG AGG CTC TTC
```

FIGURE 17V (CONT.)

```
A    N    L    W    G    R    L    E    E    E    R    L    L    W    L    Y    R
GCC  AAC  CTG  TGG  GGG  AGG  CTT  GAG  GAG  GAG  AGG  CTC  CTT  TGG  CTT  TAC  CGG

E    V    E    R    P    L    S    A    V    A    L    M    E    A    T    G    V
GAG  GTG  GAG  AGG  CCC  CTT  TCC  GCT  GTC  GCC  CTG  ATG  GAG  GCC  ACG  GGG  GTG

R    L    D    V    A    Y    L    R    A    R    L    E    V    A    E    E    I
CGC  CTG  GAC  GTG  GCC  TAT  CTC  AGG  GCC  GCC  TTG  TCC  CTG  GAG  GCC  GAG  ATC

A    R    L    E    A    E    V    F    R    L    A    G    H    P    F    N    L    N
GCC  CGC  CTC  GAG  GCC  GAG  GTC  TTC  CGC  CTG  GCC  GGC  CAC  CCC  TTC  AAC  CTC  AAC

S    R    D    Q    L    E    V    R    L    F    D    E    L    G    L    P    A    I
TCC  CGG  GAC  CAG  CTG  GAC  GTC  GAA  AGG  CTC  TTT  GAC  GAG  GGG  CTT  CCC  GCC  ATC

G    K    T    E    K    T    G    K    R    S    T    A    A    V    L    E    A
GGC  AAG  ACG  GAG  AAG  ACC  GGC  AAG  CGC  AGG  TCC  ACC  AGC  GCC  GTC  CTG  GAG  GCC

L    R    E    A    H    P    I    V    E    K    I    L    Q    Y    R    E    L    T
CTC  CGC  GAG  GCC  CAC  CCC  ATC  GTG  GAG  AAG  ATC  CTG  CAG  TAC  CGG  GAG  CTC  ACC

K    L    K    S    Y    T    I    D    P    L    P    D    I    H    P    R    T
AAG  CTG  AAG  AGC  TAC  ACC  ATT  GAC  CCC  TTG  CCG  GAC  CTC  CAC  CCC  AGG  ACG

G    R    L    H    T    R    F    N    Q    T    A    T    G    R    L    S
GGC  CGC  CTC  CAC  ACC  CGC  TTC  AAC  CAG  ACG  GCC  ACG  GGC  AGG  CTA  AGT

S    D    P    N    L    Q    N    I    P    V    R    T    P    L    G    Q    R
AGC  TCC  GAT  CCC  AAC  CTC  CAG  AAC  ATC  CCC  GTC  CGC  ACC  CCG  GGG  CAG  AGG

I    R    A    F    I    A    E    E    A    W    L    L    V    A    L    D    Y
ATC  CGC  GCC  TTC  ATC  GCC  GAG  GAG  GCC  TGG  GGG  CTA  TTG  GTG  GCC  CTG  GAC  TAT

S    Q    I    E    L    R    V    L    A    H    L    S    G    D    E    N    L    I
AGC  CAG  ATA  GAG  CTC  AGG  GTG  CTG  GCC  CAC  CTC  TCC  GGC  GAC  GAG  AAC  CTG  ATC

R    V    F    Q    E    G    R    D    I    H    T    E    T    A    S    W    M    F
```

FIGURE 17V (CONT.)

```
      CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GAG ACC GCC AGC TGG ATG TTC

  G   V   P   R   E   A   V   D   P   L   M   R   A   A   K   T   I
  GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGG GCC GCG AAG ACC ATC

  N   F   G   V   Y   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
  AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

  I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
  ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

  K   V   R   A   W   I   E   K   T   R   E   G   R   R   R   G   Y
  AAG GTG CGG GCC TGG ATT GAG AAG ACC CGC GGC GGC AGG CGG CGG GGG TAC

  V   E   T   L   F   G   R   R   A   E   D   L   E   A   R   V
  GTG GAG ACC CTC TTC GGC CGC CGC GCC GAG GAC CTA GAG GCC CGG GTG

  K   S   V   R   E   A   A   E   M   A   F   N   M   P   V   Q   G
  AAG AGC GTG CGG GAG GCG GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

  T   A   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
  ACC GCC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

  E   M   G   A   R   M   L   Q   V   H   D   E   L   V   E   A
  GAA ATG GGG GCC AGG ATG CTC CAG GTC CAC GAC GAG CTC GTC GAG GCC

  P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
  CCA AAA GAG AGG GCG GAG GAG GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

  V   Y   P   L   A   V   P   L   E   V   I   G   E   D   W
  GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GGG ATA GGG GAG GAC TGG

  L   S   A   K   E   G   I   D   G   R   G   G   H   H   H
  CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGA GGC GGG CAT CAT CAT

  H   H   //  //
  CAT CAT
```

FIGURE 17V (CONT.)

```
M    P    F    E    I    V    F    E    G    A    K    E    F    A    Q    L    I    D
ATG  CCA  TTT  GAA  ATC  GTA  TTT  GAA  GGT  GCA  AAA  GAG  TTT  GCC  CAA  CTT  ATA  GAC      18
                                                                                              54

T    A    S    K    L    I    D    E    A    A    F    V    T    E    D    G    I
ACC  GCA  AGT  AAG  TTA  ATA  GAT  GAG  GCG  GCC  TTT  GTT  ACA  GAA  GAT  GGG  ATA           36
                                                                                             108

S    M    R    A    M    D    P    S    R    V    V    I    D    L    N    L    P
AGC  ATG  AGG  GCC  ATG  GAT  CCA  AGT  AGA  GTT  GTC  ATT  GAC  CTA  AAT  CTC  CCG           54
                                                                                             162

S    S    I    F    S    K    Y    E    V    E    P    E    T    I    G    V    N
TCA  AGC  ATA  TTT  AGC  AAA  TAT  GAA  GTT  GAA  CCA  GAA  ACA  ATT  GGA  GTT  AAC           72
                                                                                             216

M    D    H    L    K    K    I    L    K    R    G    K    A    D    T    L    I
ATG  GAC  CAC  CTA  AAG  AAG  ATC  CTA  AAG  AGA  GGT  AAA  GAC  ACC  TTA  ATA                90
                                                                                             270

L    K    G    E    E    N    F    L    E    I    T    I    Q    T    A    T
CTC  AAG  GGA  GAG  GAA  AAC  TTC  TTA  GAG  ATA  ACA  ATT  CAA  GGA  GCA  ACA               108
                                                                                             324

R    T    F    R    V    P    L    I    D    V    E    M    E    V    D    L    P
AGA  ACA  TTT  AGA  GTT  CCC  CTA  ATA  GAT  GTA  GAA  ATG  GAA  GTT  GAC  CTC  CCA          126
                                                                                             378

E    L    P    F    T    A    K    V    V    L    G    E    V    L    K    D    A
GAA  CTT  CCA  TTC  ACT  GCA  AAG  GTT  GTA  CTT  GGA  GAA  GTC  CTA  AAA  GAT  GCT          144
                                                                                             432

V    K    D    A    S    L    V    S    D    S    I    K    F    I    A    R    E    N
GTT  AAA  GAT  GCC  TCT  CTA  GTG  AGT  GAC  AGC  ATA  AAA  TTT  ATT  GCC  AGG  GAA  AAT     162
                                                                                             486

E    F    I    M    K    A    E    G    E    T    Q    E    V    E    I    K    L    T
GAA  TTT  ATA  ATG  AAG  GCA  GAG  GGA  ACC  CAG  GAA  GTT  GAG  ATA  AAG  CTA  ACT          180
                                                                                             540

L    E    D    E    G    L    L    D    I    E    V    Q    E    E    T    K    S    A
CTT  GAA  GAT  GAG  GGA  TTA  TTG  GAC  ATC  GAG  GTT  CAA  GAG  ACA  AAG  AGC  GCA          198
                                                                                             594

Y    G    V    S    L    S    D    M    V    K    G    L    A    D    E
TAT  GGA  GTC  AGC  TAT  CTC  TCC  GAC  ATG  GTT  AAA  GGA  CTT  GCC  GAT  GAA              216
                                                                                             648
```

FIGURE 17V (CONT.)

```
 V   T   I   K   F   G   N   E   M   P   M   Q   M   E   Y   Y   I   R       234
GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA     702

 D   E   G   R   L   T   F   L   A   P   R   V   E   E   *                   250
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA
```

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

```
ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa ctttttagacc atacatttac gctccttctca gggatgattc

aaagattgaa gaagttaaga aataacgggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aaggttgaga aaagtttct cggcaagcct attaccgtgt ggaaacttta

tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
```

FIGURE 17W (CONT.)

```
aataccaatg gaggggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat

agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact

tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca aggaagaat acatttcgac ttgtatcatg taataacaag

gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga

gagagttgcc aaatactcga tggagatgc aaaggcaact tatgaactcg ggaaagaatt

ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag

gtcaagcaca gggaacctttg tagagtggtt cttacttagg aaagcctacg aaagaaacga

agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt

tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat

ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac

aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc

gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
```

FIGURE 17W (CONT.)

```
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agtttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca ataggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
```

FIGURE 17W (CONT.)

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct

acaattttt cctgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccggggt tttgtattgc tctagccaag gttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taactttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccaggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg //

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT CCA AGT AGA GTT GTC ATT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT AAA TAT GAA GTT GTT GAA CCA GAA ACA CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA AAG AGA ATC CTA AAG AGA GGT AAA GCA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG GGA GAA AAC TTC TTA GAG ATA ACA ATT CAA GAC ACC TTA ATA   270
CTC AAG AAA GGA GAG GTT CCC CTA ATA GAT GTA GAA GAG ATG CAA GGA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCA AAG GCA AAG GTT CTT GGA GAA GTC CTA AAA GAT GCT CCA   378
GAA CTT CCA TTC ACT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT   432
GTT AAA GAT GAT GCC TCT CTA GTG AGT GAC AGC ACC CAG GAA GTT GAG ATA AAG CTA ACT   486
GAA TTT ATA ATG AAG GCA GGA TTA TTG GAC ATC GAG GTT CAA GGA ACA AAG AGC GCA   540
CTT GAA GAT GAG GGA TTA TTG GAC ATC TCC GAC ATG GTT AAA GGA CTT GGA ACA AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC AAT GAA ATG CCC ATG CAA ATG GCC GAT TAC ATT GAA   648
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA   702

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC        54
ACC GCA AGT AAG TTA ATA GAT GAT CCA AGT GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC ATT GAC CTG ATT GAC ACA AAT CTC CCG   162
TCA AGC ATA TTT AAA CTA AAG AAG GAA AAC TAT GAA AAA CCA GAA ACA ATT GGA GTT TTA   216
ATG GAC AAA GAC GAG CAC CTA AGG AGA ATC TTA GAG ATT ACA GGA ACC TTA ATA   270
CTC AAG AAA GGA GTT CCC CTA ATA AAG GTA AAG AGA ATC CAA AGT GAA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCA GCA AAG GTA GTT GTT CTT GGA GTC CTA AAA GAT GCT CCA   378
GAA CTT CCA TTC ACT GCA TTC GTG AGT GAG AAA AGC ATT GCC AGG GAA GAT GCT CCA   432
GTT AAA GAT GCC TCT CTA CTA AAG ATA ACC CAG GAA GTT ATA AAG CTA ACT AAT   486
GAA TTT ATA ATG AAG GCA GAG GGA TTA TTG GAC TTC GTT AAA GAG GAG ACA AAG AGC ACT   540
CTT GAA GAT GAG AGC TTG TCC GAC ATG GTT AAA GGA CTT AAA ATG CCC GAT GCC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC AAT GAA ATG AAA ATG CCC ATG AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT TTC CTA CTG GCT CCA AGA GTT GAA TAT TAC ATT AGA GAG   702
GAT GAA GGA AGA CTT ACA AGA TTC ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG
```

```
ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
```

FIGURE 17X (CONT.)

```
taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta

tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat

agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact

tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca agggaagaat acattcgac ttgtatcatg taataacaag

gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga

gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

ccttccaatg gaaattcagc ttccaagatt agttggacaa cctttatggg atgtttcaag

gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga

agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
```

FIGURE 17X (CONT.)

```
tagagccta   tatccctcga  ttataattac  ccacaatgtt  tctcccgata  ctctaaatct

tgagggatgc  aagaactatg  atatcgctcc  tcaagtaggc  cacaagttct  gcaaggacat

ccctggtttt  ataccaagtc  tcttgggaca  tttgttagag  gaaagacaaa  agattaagac

aaaaatgaag  gaaactcaag  atcctataga  aaaaatactc  cttgactata  gacaaaaagc

gataaaactc  ttagcaaatt  ctttctacgg  atattatggc  tatgcaaaag  caagatggta

ctgtaaggag  tgtgctgaga  gcgttactgc  ctgggaaga   aagtacatcg  agttagtatg

gaaggagctc  gaagaaaagt  ttggatttaa  agtcctctac  attgcacctg  atggtctcta

tgcaactatc  ccaggaggag  aaagtgagga  aataaagaaa  aaggctctag  aatttgtaaa

atacataaat  tcaaagctcc  ctggactgct  agagcttgaa  tatgaagggt  tttataagag

gggattcttc  gttacgaaga  agaggtatgc  agtaatagat  gaagaaggaa  aagtcattac

tcgtggttta  gagatagtta  ggagagattg  gagtgaaatt  gcaaaagaaa  ctcaagctag

agttttggag  acaatactaa  aacacggaga  tgttgaagaa  gctgtgagaa  tagtaaaaga

agtaatacaa  aagcttgcca  attatgaaat  tccaccagag  aagctcgcaa  tatatgagca

gataacaaga  ccattacatg  agtataaggc  gataggtcct  cacgtagctg  ttgcaaagaa

actagctgct  aaaggagtta  aaataaagcc  aggaatggta  attggataca  tagtacttag

aggcgatggt  ccaattagca  ataggcaat   tctagctgag  gaatacgatc  ccaaaaagca

caagtatgac  gcagaatatt  acattgagaa  ccaggttctt  ccagcggtac  ttaggatatt

ggagggattt  ggatacagaa  aggaagacct  cagataccaa  aagacaagac  aagtcggcct

aacttcctgg  cttaacatta  aaaaatccta  gaaaagcgat  agatatcaac  tttattctt
```

FIGURE 17X (CONT.)

```
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttattta

tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttcctctgg ctcggaanng gaggattcat aacaacagta tcaacattct

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct

acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccgggagt tttgtattgc tctagccaag gttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taactttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg // TGA
```

FIGURE 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 67) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC       54
ACC GCA AGT AGG TTA ATA GAT GAG GCG TTT AAA GTT ACA GAA GAT GGG ATA          108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG      162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC      216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA ATT GAC AAG TTA ATA      270
CTC AAG AAA GGA GAG GAA AAC TTC TTA ATA GAT GTA GAA CAA GGA ACT GCA ACA      324
AGA ACA TTT AGA GTT CCC CTA AAG GTT CTT GGA GAA GTC CTA AAA GAT GCT          378
GAA CTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA TTT GCC AGG GAA AAT          432
GTT GAA TTT ATA ATG GCA GGA TTA CTC GAA GTT CAG ACC GAA GTT AAG CTA ACT      486
CTT GAA GAT GAG AGC AGC TAT CTC GAC ATC GAG GTT AAA GGA CTT GGA AAG GCC GAT GAA  540
TAT GGA GTC AGC AGC TAT TTT GGA AAT GAA ATG CCC ATG CAA ATG GCC GAT TAC ATT AGA  594
GTT ACA ATA AAG TTT GGA AAT GAA TTC CTA CTG GCT CCA AGA GTT GAA GAG //        648
GAT GAA GGA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //            702
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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAGGTG ATTACTTGGA AAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
```

FIGURE 17Y (CONT.)

```
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG  660
AAAAGGCCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //             2328
// TGA
```

Figure 17Z

PFU DNA POLYMERASE (V93 R OR E)-(PCNA) fusion protein

FIGURE 17Z (CONT.)

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAATTTAA GATAGAGCAT TTAGACCATA CATTTACGCT CATTTACGCT  120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA  180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG AGTTTCTCGG CAAGCCTATT             240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT   300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG   660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAAGTCAAGG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG TTTCGACTTG               780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT  1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA  1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG  1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC  1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT  1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC  1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA  1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT  1440
GACTATAGAC AAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT  1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG  1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT  1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG  1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT  1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAGAGA GGTATGCAGT AATAGATGAA  1800
```

```
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //               2328
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AGG GCC ATG TTA ATA GAT CCA AGT GTT GTC ACA GAA GAT GGG ATA  108
AGC ATG AGG GAT GCC ATG AGC GTT AGA GTT GTT GTC CTG ATT GAC AAT CTC CCG  162
TCA AGC ATA TTT AGC AAA AAG AAG CTA ATT GGA GTT AAC GCA ATT GGA GTT AAC  216
ATG GAC CAC CTA CTA AAG AAG GAA GAA GAG AAC TTC TTA GAG ATA GAT GCA ACA  270
CTC AAG AAA GGA GAG GTT CCC CTA AAG GTT CTA GAT GTT CTT GGA GAA ATG ATG  324
AGA ACA TTT AGA GTT CCA GCA TTC ACT GCC AAG GTT GAA GTC CTA AAA GAT GCT  378
GAA CTT AAA GAT GCC TCT CTA GTG AGT GGA GGA GAA ACC CAG GAA GTT CTA AAA  432
GTT TTT ATA GCC ATG GCA GGA TTA TTG GAC ATC GAG GTT AAA GGA CTT AAT GAA  486
GAA TTT ATA ATG ATA AAG AAG GCA GAG GAA GTT TTT GAC ATC TCC GAC ATG GAA  540
CTT GAA GTC GAC TAT CTC TCC GAC AAT GAA AAT GAA ATG GGA CTT CTT AAA GCA  594
TAT GGA GTC AGC TAT TTT GGA AAT AAT GAA ATG GGA GAT GCC GAT GAG AGC GCA  648
GAT GAA GGA AGA ACA GGA CTT ACA TTC ACA CTG CCA AGA GTT GAA GAG TGA      702
```

Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 29)   // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 30)   // Nucleotide sequence (SEQ ID NO: 67)

FIGURE 17AA (CONT.)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA    60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT   120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA   180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT   240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT   300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA AAAGAGATAC AAAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG   660
AAAAGGGCAG AAAAACTTGG GATTAAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG   780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT  1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA  1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG  1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC  1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT  1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC  1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA  1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT  1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT  1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG  1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT  1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG  1680
GCTCTAGAAT TTGTAAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT  1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGGAGA GGTATGCAGT AATAGATGAA  1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA  1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT  1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG  1980
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FIGURE 17AA (CONT.)

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CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC  54
ACC GCA AGT AGG GCC ATG GAT CCA AGT GTT GTC ATT GAC ACA GAA GAT GGG ATA  108
AGC ATG AGC ATG GAT AAA TAT GAA GTT GTT GAA CCA CCA ATT GAC CTA AAT CTC CCG  162
TCA AGC ATA TTT CTA AAG AAG ATC CTA AAG AGA GGT AAA ACC ATT GGA GTT AAC  216
ATG GAC CAC CTA AAG GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GCA TTA ATA  270
CTC AAG AAA GGA GAG GTT CCC CTA ATA GAT GTT GAA ATG ATA GAA GGA ACT GCA ACA  324
AGA ACA TTT AGA GTT CCA GCA AAG GTT CTT GGA GTC CTA AAA GAT GCT CCA  378
GAA CTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT  432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT  486
GAA TTT ATA ATG GCA GGA TTA TTG GAC GAA GTT CAG GTT GAG GAG ATA AAG CTA ACT  540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT AAA GGA CTT CAA ATG AGC GCA  594
TAT GGA GTC AGC TAT CTC TCC GAC GAA GTT AAA CCC ATG CAA ATG GCC GAT GAA  648
GTT ACA ATA AAG TTT GGA AAT GAA TTC CTA CTG GCT CCA AGA GTT GAT ATT AGA  702
GAT GAA GGA CTT ACA AGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA
```

Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)
Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

FIGURE 17BB (CONT.)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGT GTT GTC ATT GAC CTA AAT CTC CCG       162
TCA AGC ATA TTT AGC AAA TAT GAA AAG GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC AAG GTT ATA   270
CTC AAG AAA GGA GAG GAA AAC TTC TTA ATA GAT GTA GAA GTT CAA GGA GTT GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTT CTT CTT GGA GAA GTC CTA AAA GAT GCT   378
GAA CTT CCA TTC ACT GCA AAG GTT GAC AGT GAC AGC ATA AAA TTT GCC AGG GAA AAT   432
GTT AAA GAT GCC TCT CTA GTG AGT GGA GAA GAA ACC CAG GTT GTT GAG ATA CTA ACT   486
GAA TTT ATA ATG AAG GCA GGA TTA TTG GAC ATC GAG GTT CAA GAG GAG AAG AGC GCA   540
CTT GAA GAT GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   594
TAT GGA GTC AGC TAT CTC TCC GAC AAT GAA ATG ATG CCC ATG GAG CAA ATG AGA ATA   648
GAT GAA GGA AGA GAA CTT ACA TTC CTA GCT GCT CCA AGA GTT GAA GTT GAG          702
```

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA    60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT   120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA   180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT   240
ACCGTGTGGA AACTTTATTT GGAACATCCC CCACTATTAG AGAAAAAGTT             300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTAGCG    660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG   780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGAA  ATTCAGCTTT CAAGATTAGT TGGACAACCT  1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA  1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG  1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC  1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT  1260
CCGGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC  1320
```

FIGURE 17BB (CONT.)

```
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGGAAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTCCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGGATTTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG   2328
```

Figure 17CC

(PCNA)-PFU DNA POLYMERASE(D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 67)   //Nucleotide sequence (SEQ ID NO: 31)
Nucleotide sequence (SEQ ID NO: 67)   //Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT GTC CTG ATT GAC CTA AAT CTC CCG           162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
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FIGURE 17CC (CONT.)

```
ATG GAC CAC CTA AAG AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA   270
CTC AAG AAA GGA GAG GAG GAA AAC TTC TTA GAG ATA GAA ACA ATT CAA GGA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT   486
GAA TTT ATA ATG GCA GGA GGA ACC CAG GAA GTT GAG ATA AAG AGC CTA ACT   540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GAG CTT AAA AAG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GAA ATG CCC ATG AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT GAA ATG CTG GCT ACA ATG TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA GAG AGA GGA CTT CTA GCT CTG CCA AGA GTT GAA GAG //
```

```
//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT   120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA   180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT   240
ACCGTGTGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT   300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAGAGATAC   360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC   420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT   480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC   540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG   600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG   660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG   720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG   780
TATCATGTAA TAACAAGGAC AATAAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA   840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA   900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT   960
GAACTCGGGA AAGAATTCCT TCCAATGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT   1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA   1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AGCCAAGTG AAGAGGAGTA TCAAAGAAGG   1140
CTCAGGGAGA GCTACACA GTT GGATTCGTT AAAGAGCCAG AAAAGGGGGT GTGGGAAAAC   1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT   1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC   1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA   1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT   1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT   1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG   1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT   1620
```

FIGURE 17CC (CONT.)

```
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGAAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACACAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //            2328
TGA
```

Figure 17DD

PFU DNA POLYMERASE(D141A/E143A/V93R OR E) - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
```

FIGURE 17DD (CONT.)

```
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC  540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG  600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG  660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGAGTA  TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA GTT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGATA  TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //              2328
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ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA  108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG  162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA AAG ATT GGA GTT AAC  216
ATG GAC CAC CTA AAG AAG GGT AAA GCA ATT GAC ACC TTA ATA                 270
CTC AAG AAA GGA GAA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA CAA ACT GCA ACA  324
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FIGURE 17DD (CONT.)

```
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA   378
GAA CTT CCA GAT GCC TCT GCA AAG GTT CTA GTT CTT GGA GAA GTC CTA AAA GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ATA AAA TTT ATT GCC AGG GAA AAT   486
GAA TTT ATA ATG GAG GCA GAG GGA GAA ACC CAG GAA GTT GAG ATA AAG CTA ACT   540
CTT GAA GAT GTC AGC GGA TTA TTG GAC ATC GAG GTT AAA GGA CTT AAA GCC AGC GCA   594
TAT GGA GTC AGC ATA AAG TTT CTC GAC TAT TCC GAC ATG ATG GGA AAG GCC GAT GAA   648
GTT ACA ATA AAG AGA TTT GGA AAT GAA ATG CCC ATG CAA ATG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GTT TGA
```

Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein

Nucleotide sequence (SEQ ID NO: 33)   // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 34)   // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG   60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC   120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG   180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG AGTTCAGAGA AGTTCCTCGG GAGACCAGTT   240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA   300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC   360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTTATGATA   420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT TCTCCCCTAC   480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TGTGAAGGAG   540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT CTATCTGAAA   600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA   660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGAAGG CGAGCCGAAG   720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC   780
TATCCTGTGA TAAGACGGAC GATAAACCTG CGTTTGAGGC CGTTTATGAA GCTTTATGAA   840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT ACGCTGAGGC AAATAACCAC AGCCTGGGAA   900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC   960
```

FIGURE 17EE (CONT.)

```
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAGGAGGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACGAGG TACTACATTG CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA TTCTGAGAGC CGACGCCGAG CTTCGGTTAC TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT GAT CCA AGT AGT GTC CTG ATT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC ATG GAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG GAA GAA GTT CTA GAG ATA GAT GTA GAA ATT CAA GGA   270
CTC AAG AAA GGA GAA GTT CCC CTA ATA GAT GTT CTT GGA GAA GTC CTA AAA GAT GCT   324
AGA ACA TTT CCA AGA GTT ACT TCC GCC AAG GTG AGT CTA GTG GAC GGA GAA AAT   378
GAA CTT CCA AGA GTT ACT GCC AAG GTT CTT AAA GCC AGG ATA GAT GCT GAA AAT   432
GTT AAA GAT GCC TCT CTA GTG AGT GGA TTA TTG GAC GTT GAG GAA ACC CTA ACT   486
GAA TTT ATA ATG GCA GGA GGA TTA TTG GAC GAA ACC CAG GTT AAA AGC CTA ACT   540
CTT GAA GTC AGC TAT TTG TCC GAC AAT GAA ATG CCC ATG AAG GCC AGC GCA GCA   594
TAT GGA GTC AGC TAT TTT CTC GAC AAT GAA ATG CCC ATG AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA GCT TAC ACA TTC GCT CCA GCT CTG GCT GTT TAC ATT TAC AGA   702
GAT GAA GGA AGA GAA CTT GGA CTT CTA GCT GCT CTG CTG CCA AGA GTT GAA GAG TGA
```

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33)
Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA   108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA   270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA ACA ATT CAA GGA ACA GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GAA GAG ATG GAA GTT GAC CTC CCA   378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT CTT GGA GAA GTC CTA AAA GAT GCT   432
GTT AAA GAT GCC TCT CTA GTG AGT GGA GAA ACC CAG ATA AAA TTT ATT GCC AAT   486
GAA TTT ATA ATG GAG GAG GTA GTT GGA GAA CTT ATT AGG GAC CTA AAG AGC ACT   540
CTT GAA GAT GTC AGC TCC CAG ATA AAA TTT CTA AAG GAA CTA AGC GAT GAC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   648
GTT ACA ATA AAG TTT GGA AAT GAA AAT TTT GCC AGG GAT TAT TAC ATT AGA       702
GAT GAA GGA AGA AGA GGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //
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```
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG  60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
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FIGURE 17FF (CONT.)

```
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GGAGGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AGTACGCGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGCCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325
```

FIGURE 17GG

(PCNA)-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 35)
Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG, (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC      54
ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA     108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG     162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC     216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA     270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG ATA GAA ATT CAA GGA ACT GCA ACA     324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTT GTA GTT CTT GGA GAA GTT CTA CCA     378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GAC AGC ATA GAA AAA GAT GCT        432
GTT AAA GAT GCC TCT GTG AGT GGA GGA GAA ACC CAG GAA TTT ATT GCC AGG GAA AAT     486
GAA TTT ATA ATG GCA AAG GCA TTA TTG GAC ATC GAG GTT GAG GAG ACA AAG AGC ACT     540
CTT GAA GAT GAG AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA     594
TAT GGA GTC AGC TAT TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA     648
GTT ACA ATA AAG TTT GGA GAA TTT CTA CTG GCT CCA AGA GTT CCA AGA GTT GAA GAG //     702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG //               702
```

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGGCAAGC CTATAATCCG AATTTTTAAG   60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT  120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGCGA GAGACATGGA  180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGACATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA  300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT  360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT  420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT  480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGA AAAATATCGA TTTGCCGTAT  540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA  600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA  660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA  720
```

FIGURE 17GG (CONT.)

```
CCCAAGGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGGAGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT GGACTTAATT CCATACTCGG 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGCGAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAAGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AGCACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ATCCTAGAAA ATCCTAGAAA ATCCTAGAAA ATCCTAGAAA 2220
```

FIGURE 17HH (CONT.)

Nucleotide sequence (SEQ ID NO: 35)   // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 36)   // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG   60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT  120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA  180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA  300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT  360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT  420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT  480
AGTTATGCCG ATGAAGAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT  540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA  600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA  660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA  720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT  780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT  840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA  900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA  960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGCCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
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FIGURE 17HH (CONT.)

```
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCG TTT AAA GTT ACA GAA GAT GGG ATA       108
AGC ATG AGG GCC ATG AGC GAT CCA AGT AGA GTT GTC ATT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA GTT GTT GAA CCA GAA ACA ATT GGA GTT AAC   216
ATG GAC CAC CTA AAG AAG ATC CTA AAG AGA GGT AAA GCA AAG GAC ACC TTA ATA   270
CTC AAG AAA GGA GAG GAA AAC TTC TTA ATA GAT GTA GAA ATT CAA GGA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA AAG GTT CTT GGA GAA GTC CTA AAA GAT GCT   378
GAA CTT CCA TTC ACT GCA AAG GTT GTA GTT GAC AGC ATA TTT GCC AGG GAA AAT   432
GTT AAA GAT GCC TCT CTA GTG AGT GGA GAA ACC CAG GAA GTT ATA AAG CTA ACT   486
GAA TTT ATA ATG AAG GCA GGA TTA TTG GAC ATC GAG GTT CAA GAG ACA AAG AGC GCA   540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT AAA GGA CTT CAA ATG AAG GCC GAT GAA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GAA AAT GGA CTT AAG TAT TAC ATT AGA   648
GTT ACA ATA AAG TTT GGA AAT TTC ACA AGC GAG CAA ATG GTT CCC AGA GTT GAA GAG   702
GAT GAA GGA AGA GAA CTT ACA CTG GCT CTA CCA GTT GAA GAG TGA
```

Figure 17II

<u>Deep Vent- (PCNA) DNA polymerase fusion protein</u>

FIGURE 17II (CONT.)

Nucleotide sequence (SEQ ID NO: 37)   // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 38)   // Nucleotide sequence (SEQ ID NO: 67)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG          60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT         120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG         180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT         240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA         300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC         360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT         420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA         480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAAACGTGA AAAAGATCGA TCTCCCGTAC         540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG TCCTCAAGGT GATAAGGGAG                    600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT         660
AAGAGGGGCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG         720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC         780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG         840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG         900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAAATGG AGGATGCAAA GGTAACGTAC         960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC        1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTTGTACCT CCTCAGGAAG        1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG        1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAAGGGCT CTGGGAGGGG        1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA        1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC        1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA        1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT        1440
GATTACAGGC AACGGGCAAT CAAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC        1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA        1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA        1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA        1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC        1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG        1800
GAAGGGGAAGA TAATCACTAG GGGGGCTTGAA ATAGTCAGGA ATAGTCAGGA GGGACTGGAG         ...
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```
                                                                     1860
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FIGURE 17II (CONT.)

```
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA   1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG   1980
CTAGTTATTT ACGAGCAGAT CACGAGCCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC   2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA   2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT   2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCACGA AGAAG //                2328
```

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCG TTT AAA GTT ACA GAT GGG ATA           108
AGC ATG AGG GCC ATG GAT CCA AGT AGT GTT GTC ATT GAC CTA AAT CTC CCG       162
TCA AGC ATA TTT AGC AAA AAG AAG ATC CTA GAA ACA ATT GGA GTT AAC           216
ATG GAC CAC CTA AAG GAG GAA AAC TTC TTA GAG ATA GCA GAC ACC TTA ATA       270
CTC AAG GAA AAA GGA GAA GTT CCC CTA ATA GAT GTA GAA GTT CAA GGA ACA       324
AGA ACA TTT AGA GTT CCA CTA ATA GAT GTA GTT CTT GGA GAA GTC GAC CTC CCA   378
GAA CTT AAA GAT GCC TCT CTA GTG AGT GAC AGC ACC CAG GAA ATA TTT GCT       432
GTT TTT ATA ATG AAG GCA GGA GGA GAA ACC ATA AAA TTT ATT GCC AGG GAA AAT   486
GAA TTT ATA ATG GCA GAG GAG CTT GAG GTT CAG GTT AAA GGA ATA AAG CTA ACT   540
CTT GAA GAT GAG AGC GCA GGA CTT AAA AGA GGA CTT GGA ACA AAG AGC GCA       594
TAT GGA GTC TAT TCC GAC ATG AAT GAA ATG GCC GAT GAA GCC GAT GAA          648
GTT ACA ATA AAG TTT GGA AAT GAT GAA ATG CCC ATG CAA GTT TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA
```

Figure 17JJ

(PCNA) - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)
Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38)

FIGURE 17JJ (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC    54
ACC GCA AGT AAG TTA ATA GAT GAG GCG TTT AAA GTT ACA GAA GAT GGG ATA       108
AGC ATG AGG GCC ATG GAT CCA AGT AGA GTT GTC CTG ATT GAC CTA AAT CTC CCG   162
TCA AGC ATA TTT AGC AAA TAT GAA ATT GTT GAA CCA GAA ACA AAG GAC GTT AAC   216
ATG GAC CAC CTA AAG AAG GAA ATC CTA AAG AGA GGT ATA GCA GAC ACC TTA ATA   270
CTC AAG AAA GGA GAG GAA AAC TTC TTA GAG GTA GAG ATT CAA GGA ACT GCA ACA   324
AGA ACA TTT AGA GTT CCC CTA ATA GAT GTA GTT CTT GGA GAA GTC CTA GAT CCA   378
GAA CTT CCA GCA TTC ACT GCA AAG GTT GTT CTT GAC AGC ATA AAA GAT GCT       432
GTT AAA GAT GCC TCT GTG AGT GGA GGA GCA GAA TTT ATT GCC AGG GAA AAT       486
GAA TTT ATA ATG AAG GCA GGA TTA TTG GAC ATC GAG GTT CAA GTT CTA ACT       540
CTT GAA GAT GAG AGC TAT CTC TCC GAC GTT AAA GGA CTT AAG AAG AGC GCA       594
TAT GGA GTC AGC TAT TTC GGA AAT TTT GAC GAA ATG GGC GAT TAC GAT GAA       648
GTT ACA ATA AAG TTT GGA AAT ATG ATG CCA AGA GTT TAC ATT AGA //           702
```

```
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG AGTTCCTGGG GAGGCCGATT GGATAAGATA   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA   300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA TATAATGATA TCTCCCGTAC   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG CCCCTGGGAA GGGACGGTAG TGAGCCAAAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAAGGATACA CTTTGACCTC AGTTTATGAG   780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA AGATAGCTGA GGCCTGGGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG AGGATGCAAA TATTCAATGG GGTAACGTAC   960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG CAAGGTTAGT GCCCAGCTTT CGGCCAGCCC  1020
```

FIGURE 17JJ (CONT.)

```
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG 1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG 1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC 1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA 1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT 1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC 1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAGAA AGTATGCGTT GATAGATGAG 1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGTCCGCAC 2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG 2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA             2328
```

Figure 17KK

<u>JDF-3 - (PCNA) fusion protein</u>

Nucleotide sequence (SEQ ID NO: 39)   // Nucleotide sequence (SEQ ID NO: 67)
Nucleotide sequence (SEQ ID NO: 40)   // Nucleotide sequence (SEQ ID NO: 67)

FIGURE 17KK (CONT.)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGAAAGCCCGTCACGAGGGTCTTCAGGAGGTTCTTCAAGAAGGAGAACGGCGAGTTCAGGAGTTCAGGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGGACGACTCTCGTCCATCGAGAGAATCAAAAGATAACCGGCGGAGGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGCGAGAAGGTGAAGAAAAGTTCCTCGG
CAGGTCTGTGGAGGTCTGGGTCCTCTACTTCACGCACCGCAGGAGCCAATCCGGACAAAATAAGAGGAGACTTAAGGAGCTAAACTCAGTACGACATACCC
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGAGCTTAAACTCATGTCCTTGₐₐGₐCGCTCTACCACGAGGGAGAAGAGTTTGGAA
CCGGGCCGATTCTGATGATAAGCTACGCCGATGGAGGCGGCGGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGGAGATGATTAA
GGGGCTTCTTGAGGGTCGTTAAGGAGGAGGACGGGCCGACGTGCTGATAACATACAACGCGGTCGAGGTGGACAGGTTTGCGTGTGAAAAAGCGCTGTGTGAGAGCTTGGCGTGAGCTTT
ACCCTCGGGAGGAGGGCGAGGGCCGAAGATACAGCGCCATGGCGGTTTCGGCAAGCCCATGGGGTACACTTGACCTTTATCCAGTAAGGCGCACCATAA
ACCTCCCGGACCCTACACCCTTGAGGCTGTATACGGAGGCGGTGTTTCGGCAAGCTGGCCTACGCGAGGGCCCAGGCCCTCTGGGAGACCCTTGAGAG
GGTCGCGCGCTACTCGGATGGGAGGACGCGCGAGTTGGTCCTCCTCGAGTGGTTCCTCCTGGGAAGCCTACGAGGAGCGAACCTGCTCCCAACAAGCCCGAGGGGGCT
CGCTCCAGCACCGGCCAACCTCGTCGAGTCCTCAAGGAGCCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTAGACTCTGCGCCAGATAC
ACgCCGGTGGCTACGTGGAGGGGTGTAGGAGCGGGACGTGCCCGAGTCGGTCACGACGTTCTGCAAGACTTCTGCAAGAGACTTCCCGGAACCTGCTGGAGGAAAGG
GTCAACCGCGAGGGGTGTAGGGGTCTACGACGTCTGGGAGGAAGAATCTCGACCCGCTGGAGAAGAATCTCGATTACAGCCAACAGCTACTACGGCTACTACGGCT
CAGAAGATAAAGAGGAAGATGAAGCAACTCTTCGCCAATCTCCTGATTACAGGACAACTCTCCTGATTACAGGGAGTCATCAGAGAGCTTGAGGAAAAAGTTCGGTTTTAAAGTCCT
ATGCCAGGGCAAGAGATGGTACTGCAGGGAGTGCGCCAGAGAGCGTTACGGACGCGTTACGGACGTTACGGACGTTACGGACGACTTCTTAAACTGTCATCAGAGAGTTCTTAAACTCATCAATCCCAAACTGCCCGGCCTTCTC
CTATGCAGAACACAGACGGTCTCCATCCAGCCCACCATTCTCAGGGGCTTCTCTACGTCAGGGCGAGGGTTTCGTGTCCGTCACGGAGGCGGCCTTGAGATAGTCAGGCGCG
GAACTCGAATACGAGGGCTTCTACGTGAAGGAGACGCAGGGCGAGGGTTTGAGGGGTTTGAGGCGAGAGATAACCACGCGGCGCTTGAGGAAGTCAGGGGCTTGAGATAGTCAGGCGCG
ACTGGAGCGAGATAGCCGAAGGAGACGCAGGGTGTATCCGAGGAGAAGCGGCTGAGAAGCTGAGCAA
GTACGAGGTTCCGCCGGAAGGTTCGCCGGAAGTGGTTATCCACGAGAGCTTCAAGGGCTCAAGGGGCTCCGGAAGGATAGGCGACAGGGCCATAGCGAGCGTTTGGCCGCAGAGGT
GTTAAATCCGGCCGGAAGTAAGAACTGTGATAAGCTACTACATCGTTCCGCCAGAGGAGATCCTCGGCAGTTGAGAGAGAATCCTCGGCAGTTGAGAGAGAAGACTCGCGCCAAGACTACGATG
CGGACTACTACCCAGGTTCTGCCGGAAGAACCAGGTTCTGCCGGAAGAACCTGGCTACGAGAAGAGAGGCCAGGTCGGCGCTTGGCGC
GTGGGCTGAAGCCCGAAGGGGAAGAAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC   54
ACC GCA AGT AGG ATG GCC ATG GAT CCA AGT GTT GTC ATT GAC CTA AAT CTC CCG   108
AGC ATG ATG AGC ATA TTT AGC ATG AAA TAT GAA GTT GTT GAA CCA GTT AAC   162
TCA AGC ATA TTT AGC AGT GAA TAT CTA AAG GTT GTT GAA CCA GTT GTT AAC   216
ATG GAC AAA GGA GAG GAA AAC TTC ATA ATA GAG AAA GCA GAC ACC TTA ATA   270
CTC AAG AAA GGA GTT CCC CTA CTA GAT GTA GAA ATG GAA GTT CAA GCA ACA   324
AGA ACA TTT AGA TTC GCA AAG GTT CTA GAT GTT CTT GGA GAA GTC CTA CCA   378
GAA CTT CCA GTT GCC CTA CTA GTA GTT GAC AGC ATA AAA TTT GCC AGG GAT GCT   432
GTT TTT ATA GAT GCC TCT AAG GCA GCA ACC CAG GAA ATA GTT GAG GAG CTA ACT   486
GAA TTT ATA ATG GAG GGA TTA GAC ATC GAG GTT CAA GTT ACA ACA AAG GCA AAT   540
CTT GAA GAT GAG GGA TTA TTG GAC ATC GAG GTT CAA GTT ACA ACA AAG AGC GCA   594
TAT GGA GTC AGC TAT CTC TCC GAC ATG GTT AAA GGA CTT GGA AAG GCC GAT GAA   648

FIGURE 17KK (CONT.)

GTT ACA ATA AAG TTT GGA AAT GAA ATG CCC ATG CAA ATG GAG TAT TAC ATT AGA   702
GAT GAA GGA AGA CTT ACA TTC CTA CTG GCT CCA AGA GTT GAA GAG TGA

Figure 17LL

(PCNA) - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 67)   // Nucleotide sequence (SEQ ID NO: 39)
Nucleotide sequence (SEQ ID NO: 67)   // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATG	CCA	TTT	GAA	ATC	GTA	TTT	GAA	GGT	GCA	AAA	GAG	TTT	GCC	CAA	CTT	ATA	GAC	54
ACC	GCA	AGT	AAG	TTA	ATA	GAT	GAG	GCC	GCG	TTT	AAA	GTT	ACA	GAA	GAT	GGG	ATA	108
AGC	ATG	AGG	GCC	ATG	GAT	CCA	AGT	AGA	GTT	GTC	ATT	GAC	CTA	AAT	CTC	CCG		162
TCA	AGC	ATA	TTT	AGC	AAA	TAT	GAA	GTT	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
ATG	GAC	CAC	CTA	AAG	AAG	ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG	GAC	ACC	TTA	ATA	270
CTC	AAG	AAA	GGA	GAG	GAA	AAC	TTC	TTA	GAG	ATA	GAA	GGA	ATG	GGA	ACT	GCA	ACA	324
AGA	ACA	TTT	AGA	GTT	CCC	CTA	ATA	GTT	CTT	GGA	GAA	GTT	GAC	CTC	CCA			378
GAA	CTT	CCA	TTC	ACT	GCA	AAG	GTT	GTA	AGT	GAC	AGC	ATA	AAA	TTT	ATT	GCC	AGG	GAA	AAT	GCT	432
GTT	AAA	GAT	GCC	TCT	CTA	GTG	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	486
GAA	TTT	ATA	ATG	AAG	GCA	TTA	GAC	ATC	GAG	GTT	CAA	GGA	CTT	GGA	ACA	AGC	GCA	540
CTT	GAA	GAT	GAG	GGA	TTA	TTG	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	GCC	GAT	GAA	594
TAT	GGA	GTC	AGC	TAT	CTC	TCC	GAC	ATG	GTT	CCC	ATG	CAA	AAG	GAG	TAT	TAC	AGA	648
GTT	ACA	ATA	AAG	TTT	GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG	TAT	TAC	ATT	AGA	702
GAT	GAA	GGA	AGA	CTT	ACA	TTC	CTA	CTG	GCT	CCA	AGA	GTT	GAA	GAG	//			

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCACTCGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCC
CTACTTCTACGGCGTCCTCAGGGACGACTTCTGCCATCGAAGAAATCAAAAAGATAACCGGCGGAGAGGCACGGCGGCAATCCGGACTACTTCCCGAGGAAGAGGTGA
AGAAAAGTTCCTCGGCAGTTCGTGAGGTCTGGGTCCTCTACTTCACGCACCGCAGGACXXXCCGGAAGCAATCCGGACACXXXCCGGATGAAGAGCTTAAACTCATGTCCTTqGAGATCGA
GACAATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGAGCTTAAACTCATGTCCTTqGAGATCGA
qACGGCTCTACCACGAGGGAGAAGAGAGTTTGGAACCGGCCGATTCTGATGATGATAAGCTACGCGCCGATGAAAAGCTACGCGCCGATGAAAAGCGAGGCGCCGTGATAACCTGGAAGAGATCGACCTTC

FIGURE 17LL (CONT.)

CTTACGTTGAGGTTGTCTCCACCGAGAAGGAGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGACGTGCTGATAACATACAACGGCGACAACTTC
GACTTCGCCTACCTGAAAAAGCGCTGTGAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTTACCCTGCGGGAGGACGGAGCGAGCCGAAGATACAGCGCATGGGGACAGGTTTGCGGT
CGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTCGGCAAGC
CCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAG
CTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCCGGCTCATCGGCCACCGGCAACCTCGTCGAGTGGTTCCT
CCTAAGGAAGGCCTACGAGAAGAACGAACTCGCTCCCAACAAGCCCGACGAGGAGAAGGGGGGCTACgccGGTGGCTACGTCAAGGAGCCGG
AGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTAC[CCT]TCAATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGTGT
AGGAGCTACGACGTTGCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCCCCGGCTTCCCCGGCTTTACGGCAAAGTTCGGCGAAGATAAA
GAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACGAGG[GCA]TCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTATG
CCAGGGCAAGAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAA
GTCCTCTATGCGAGACACAGACGGTCTCCATGCCACCATTCGTGGAGCGGACGCGTGAAACAGTCAAGAAAAAGCAATGGAGTTCTTAAACTATATCAATCCCAAACT
GCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGTCATCGACGAGGAGGGCAAGATAACCACGCGCG
GGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGACGGAGGGTTTGGAGGCGATACTCAGGCACGTGACGTTGAAGAGGCCGTCAGAATT
GTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAAGACTACCAAGGCCACCGGCCC
GCACGTAGCCATAGCGAAgCGTTTGGCGCCGACCGGAGGTGTTAAAATCCGGCCCGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGG
CGATTCCCTTCGACGAGTTCGACCCCGACCAGAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGC
TACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCCAGGTCGGGGCTTGGCGCGTGGCTGA

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Figure 17MM

Sac7d gene (ACCESSION No: M87569)

Nucleotide sequence (SEQ ID NO: 69)
Amino acid sequence (SEQ ID NO: 70)

```
 M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S     18
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA    54

 K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D     36
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC   108

 N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L     54
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA   162

 L   D   M   L   A   R   A   E   R   E   K   K   *                        67
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA TAA                       201
```

Figure 17NN

Sac7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)
Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66)

```
 M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA

 K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

 N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
```

FIGURE 17NN (CONT.)

```
 L   D   M   L   A   R   A   E   R   E   K   K   //
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

 G   G   G
// GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC GTG

 D   G   H   H   L   A   Y   R   T   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S   R   G   E   P   V   Q   A   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A   L   K   D   D   G   A   V   I   V   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG GTC TTT GAC GCC AAG GCC CCC

 S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   T   P
TCC TTC CGC CAC GAG GCC TAC TAC GGG GGG TAC AAG GCG GGC CGG GCC ACG CCA

 E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

 L   A   R   L   E   V   P   G   Y   E   A   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GTC CTG GCC AGC CTG

 A   K   K   A   E   K   E   G   Y   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG TAC CGC GTC GAG CTC ACC GCC GAC AAA

 D   L   Y   Q   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

 L   I   T   P   A   W   L   W   E   K   Y   G   L   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC GAC CAG TGG

 A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
```

FIGURE 17NN (CONT.)

```
      A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
     GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

  G   I   G   E   K   T   A   R   K   L   E   L   E   W   G   S   L   E
 GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT GAG CTG GAG TGG GGG AGC CTG GAA

  A   L   K   N   L   D   R   L   K   A   I   R   E   K   I   E   I   L
 GCC CTC AAG AAC CTG GAC CGG CTG AAG GCC ATC CGG GAG AAG ATC GAG ATC CTG

  A   H   M   D   D   L   S   W   D   L   A   V   K   V   R   T   D
 GCC CAC ATG GAC GAT CTG AGC TGG GAC CTG GCC GTG AAG GTG CGC ACC GAC

  L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
 CTG CCC CTG GAG GTG GAC TTC GCC AAA CGG AGG GAG CCC GAC CGG GAG CGG CTT

  R   A   F   L   E   R   E   F   G   S   L   H   E   F   G   L
 AGG GCC TTT CTG GAG CGG GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT

  L   E   S   P   K   A   A   L   E   E   P   P   E   G   A
 CTG GAA AGC CCC AAG GCC GCC CTG GAG GAG CCG CCC GAA GGG GCC

  F   V   G   F   V   L   S   R   S   K   E   K   M   W   P   D   L   A
 TTC GTG GGC TTT GTG CTT TCC CGC AGC AAG GAG AAG ATG TGG CCC GAT CTT GCC

  L   A   A   A   R   G   R   V   H   R   A   P   E   P   Y   K   A
 CTG GCC GCC GCC AGG GGG CGG GTC CAC CGG GCC CCG GAG CCT TAT AAA GCC

  L   R   D   L   K   E   A   R   G   L   L   A   K   D   L   S   V   L
 CTC AGG GAC CTG AAG GAG GCC CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

  A   R   E   G   L   G   L   P   P   D   D   D   P   M   L   L   A
 GCC AGG GAA GGC CTT GGC CTC CCG CCC GAC GAC GAC CCC ATG CTC CTC GCC

  Y   L   D   P   S   N   T   T   P   E   G   V   A   R   R   Y   G
 TAC CTC GAC CCT TCC AAC ACC ACC CCC GAG GGG GTG GCC CGG CGC TAC GGC

  G   E   T   E   E   A   G   E   R   A   A   L   S   E   R   L   F
 GGG GAG ACG GAG GAG GCG GGG GAG CGG GCC GCC CTT TCC GAG AGG CTC TTC
```

FIGURE 17NN (CONT.)

```
A   N   L   W   G   R   L   E   G   E   E   R   L   L   W   L   Y   R
GCC AAC CTG TGG GGG AGG CTT GAG GGG GAG GAG AGG CTC CTT TGG CTT TAC CGG

E   V   E   R   P   L   S   A   V   L   A   H   M   E   A   T   G   V
GAG GTG GAG AGG CCC CTT TCC GCT GTC CTG GCC CAC ATG GAG GCC ACG GGG GTG

R   L   D   V   A   Y   L   R   A   E   V   F   R   L   A   E   E   I
CGC CTG GAC GTG GCC TAT CTC AGG GCC GAG GTC TTC CGC CTC AGG GCC GAG ATC

A   L   E   A   L   R   F   V   E   A   L   G   H   L   P   A   E   I
GCC CTC GAG GCC CTC CGC TTC GTC GAG GCC CTG GGC CAC CTA CCC GCC GAG ATC

S   R   D   Q   L   E   V   R   E   S   T   S   A   V   L   E   L   T
TCC CGG GAC CAG CTG GAA GTC AGG GAA TCC ACC TCC GCC GTC CTA GAG CTG ACC

G   K   T   E   K   R   T   G   K   R   S   A   T   K   E   S   A   T
GGC AAG ACG GAG AAG CGC ACC GGC AAG CGC AGC GCC ACC AAG GAG AGC GCC ACG

L   R   E   A   H   P   I   V   E   K   I   L   Y   R   E   L   R   T
CTC CGC GAG GCC CAC CCC ATC GTG GAG AAG ATC CTG TAC CGG GAG CTC AGG ACG

K   L   S   T   Y   I   Y   S   K   P   D   L   I   P   H   R   P   T
AAG CTG AGC ACC TAC ATT TAC AGC AAG CCC GAC CTC ATC CCG CAC CAC CCC ACG

G   R   H   T   A   Q   I   A   E   V   Q   L   D   P   A   T   G   L
GGC CGC CAC ACC GCC CAG ATC GCC GAG GTG CAG CTG GAC CCG GCC ACG GGC CTA

S   D   P   N   L   A   N   L   Q   A   E   E   G   D   E   N   L   S
AGC GAT CCC AAC CTC GCC AAC CTC CAG GCC GAG GAG GGG GAC GAG AAC CTA AGT

I   R   A   F   I   R   R   A   I   E   I   W   A   L   V   A   D   Y
ATC CGC GCC TTC ATC CGG CGC GCC ATC GAG ATC TGG GCC CTG GTG GCC GAC TAT

S   Q   I   E   L   R   A   F   L   R   H   S   G   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GCC TTC CTC CGG CAC TCC GGC GAC GAG AAC CTG ATC

R   V   F   Q   E   G   R   D   I   H   T   A   S   W   M   F
CGG GTC TTC CAG GAG GGG CGG GAC ATC CAC ACG GCC AGC TGG ATG TTC
```

FIGURE 17NN (CONT.)

```
G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

N   F   G   V   L   Y   G   M   S   A   H   R   L   R   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC CGG GAG CTA GCC

I   P   Y   E   E   A   Q   A   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG GCC TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   R   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG TAC

V   E   T   L   F   G   R   R   R   Y   V   P   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   G
AAG AGC GTG CGG GAG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC GGC

T   A   D   L   M   K   L   A   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E   M   G   A   R   M   L   Q   V   H   D   E   L   V   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAG CTG GTC CTC GAG GCC

P   E   R   A   E   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   L   A   V   P   L   E   V   G   I   G   E   E   D   W
GTG TAT CCC CTG GTG CCC CTG GAG GTG GGG ATA GGG GAG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
CTC TCC GCC AAG GAG ATT GAT GGC CGC GGA GGC GGG CAT CAT CAT

H   H   *
CAT CAT TAA
```

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Figure 1700

Taq DNA polymerase- Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)
Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70)

```
       G   G   G
    // GGC GGC GGT

 V   T   S   G   M   L   P   L   F   E   P   K   G   R   V   L   L   V
GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG GTG

 D   G   H   H   L   A   Y   R   T   F   F   H   A   L   K   G   L   T   T
GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC

 S   R   G   E   P   V   Q   A   V   Y   G   F   A   K   S   L   L   K
AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG

 A   L   K   E   D   G   D   A   D   V   I   V   F   D   A   K   A   P
GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG TTT GAC AAG GCC AAG GCC CCC

 S   F   R   H   E   A   Y   G   G   Y   K   A   G   R   A   P   T   P
TCC TTC CGC CAC GAG GCC TAC GGG TAC AAG GCG GGC CGG GCC CCC ACG CCA

 E   D   F   P   R   Q   L   A   L   I   K   E   L   V   D   L   L   G
GAG GAC TTT CCC CGG CAA CTC GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG

 L   A   R   L   E   V   P   G   Y   E   A   D   D   V   L   A   S   L
CTG GCG CGC CTC GAG GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG

 A   K   K   A   E   K   E   G   Y   E   V   R   I   L   T   A   D   K
GCC AAG AAG GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA
```

FIGURE 1700 (CONT.)

```
D   L   Y   Q   L   L   S   D   R   I   H   V   L   H   P   E   G   Y
GAC CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG TAC

L   I   T   P   A   W   L   Y   K   E   R   P   D   Q   W
CTC ATC ACC CCG GCC TGG CTT TAC AAG GAA GGC CTG AGG CCC GAC CAG TGG

A   D   Y   R   A   L   T   G   D   E   S   D   N   L   P   G   V   K
GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC CTT CCC GGG GTC AAG

G   I   G   E   K   T   A   R   K   L   L   E   E   W   G   S   L   E
GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG GAG GAG TGG GGG AGC CTG GAA

A   L   K   N   L   D   R   L   K   P   A   I   R   E   K   I   L
GCC CTC AAG AAC CTG GAC CGG CTG AAG CCC GCC ATC CGG GAG AAG ATC CTG

A   H   M   D   D   L   K   L   S   W   D   A   L   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC GCC CTG AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   E   R   E   P   D   R   E   R   L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG GAG CGG GAG CCC GAC GAG AGG CTT

R   A   F   L   E   R   L   E   F   G   S   L   L   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC AGC CTC CAC GAG TTC GGC CTT

L   E   S   P   K   A   L   E   E   A   P   W   P   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG GCC CCG TGG CCC CCG GAA GGG GCC

F   V   G   F   V   L   S   R   K   E   P   M   W   A   D   L   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG ATG CCC ATG TGG GCC GAT CTT CTG GCC

L   A   A   R   G   G   R   V   H   R   A   P   E   Y   K   A
CTG GCC GCC AGG GGG GGC GTC CAC CGG GCC CCC GAG CCT TAT AAA GCC

L   R   D   L   K   E   A   R   G   L   L   D   K   D   L   S   V   L
CTC AGG GAC CTG AAG GAG GCG CGG GGG CTT CTC GCC AAA GAC CTG AGC GTT CTG

A   L   R   E   G   L   P   P   D   D   P   M   L   L   A
GCC CTG AGG GAA GGC CTT GGC CCC GGC GAC GAC ATG CTC CTC GCC
```

FIGURE 1700 (CONT.)

```
Y    L    D    P    S    N    T    T    P    E    G    V    A    R    R    Y    G
TAC  CTC  GAC  CCT  TCC  AAC  ACC  ACC  CCC  GAG  GGG  GTG  GCC  CGG  CGC  TAC  GGC

G    E    W    T    E    E    A    G    E    R    A    L    S    E    R    L    F
GGG  GAG  TGG  ACG  GAG  GAG  GCG  GGG  GCC  CGG  GCC  CTT  TCC  GAG  AGG  CTC  TTC

A    N    L    W    G    L    E    G    E    E    W    L    L    E    R    Y    R
GCC  AAC  CTG  TGG  GGG  AGG  GAG  GGG  GAG  GAG  TGG  CTC  CTT  TGG  TAC  CGG

E    V    E    R    P    L    S    A    V    L    A    H    M    E    A    T    G    V
GAG  GTG  GAG  AGG  CCC  CTT  TCC  GCT  GTC  CTG  GCC  CAC  ATG  GAG  GCC  ACG  GGG  GTG

R    L    D    V    A    Y    L    R    A    L    S    L    E    V    A    T    E    I
CGC  CTG  GAC  GTG  GCT  TAT  CTC  AGG  GCC  TCC  GTG  TTG  CTG  GAG  GTC  ACG  GAG  ATC

A    L    E    A    E    V    F    R    L    A    G    H    P    F    N    L    N
GCC  CTC  GAG  GCC  GAG  GTG  TTC  CGC  CTG  GCC  GGC  CAC  CCC  TTC  CTC  AAC

S    D    Q    L    E    R    V    E    D    F    L    E    L    G    L    P    A    I
TCC  GAC  CAG  CTG  GAA  AGG  GTC  TTT  GAC  CTC  GAG  CTA  GGG  CTT  CCC  GCC  ATC

G    K    T    E    K    T    G    K    R    S    T    A    V    L    E    A
GGC  ACG  GAG  AAG  AAG  ACC  GGG  AAG  CGC  TCC  ACC  AGC  GCC  GCC  GTC  CTG  GAG  GCC

L    R    E    A    H    P    I    V    E    K    I    L    Q    Y    R    E    L    T
CTC  CGC  GAG  GCC  CAC  CCC  ATC  GTG  GAG  AAG  ATC  CTG  CAG  TAC  CGG  GAG  CTC  ACC

K    L    K    S    T    Y    I    D    P    L    D    L    P    I    H    P    R    T
AAG  CTG  AAG  AGC  ACC  TAC  ATT  GAC  CCG  TTG  GAC  CTC  CCG  ATC  CAC  CCC  AGG  ACG

G    R    L    T    T    N    R    Q    T    A    T    A    G    R    L    S
GGC  CGC  CTC  ACC  ACG  AAC  TTC  CAG  ACG  GCC  ACG  GCC  GGC  AGG  CTA  AGT

S    D    P    N    L    Q    I    P    V    R    T    P    L    Q    G    R
AGC  TCC  GAT  CCC  AAC  CTC  CAG  AAC  ATC  CCC  GTC  ACC  CCG  CTT  GGG  CAG  AGG

I    R    A    F    I    A    E    E    G    W    L    L    V    A    L    D    Y
```

FIGURE 1700 (CONT.)

```
I   R   R   A   F   I   A   E   E   G   W   L   L   V   A   L   D   Y
ATC CGC CGG GCC TTC ATC GCC GAG GAG GGG TGG CTA TTG GTG GCC CTG GAC TAT

S   Q   I   E   L   R   V   L   A   H   G   S   D   E   N   L   I
AGC CAG ATA GAG CTC AGG GTG CTG GCC CAC GGC TCC GAC GAG AAC CTG ATC

R   F   V   F   Q   E   R   G   E   R   T   H   T   A   S   W   M   F
CGG TTC GTC TTC CAG GAG CGG GGG GAG CGG ACC CAC ACG GCC AGC TGG ATG TTC

G   V   P   R   E   A   V   D   P   L   M   R   R   A   A   K   T   I
GGC GTC CCC CGG GAG GCC GTG GAC CCC CTG ATG CGC CGG GCG GCC AAG ACC ATC

N   F   G   V   L   Y   G   M   S   A   H   R   L   S   Q   E   L   A
AAC TTC GGG GTC CTC TAC GGC ATG TCG GCC CAC CGC CTC TCC CAG GAG CTA GCC

I   P   Y   E   E   A   Q   F   I   E   R   Y   F   Q   S   F   P
ATC CCT TAC GAG GAG GCC CAG TTC ATT GAG CGC TAC TTT CAG AGC TTC CCC

K   V   R   A   W   I   E   K   T   L   E   E   G   R   R   G   Y
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC CGG AGG GGG TAC

V   E   T   L   F   G   R   R   Y   V   P   D   L   E   A   R   V
GTG GAG ACC CTC TTC GGC CGC CGC TAC GTG CCA GAC CTA GAG GCC CGG GTG

K   S   V   R   E   A   A   M   R   M   A   F   N   P   V   Q   G
AAG AGC GTG CGG GAG GCC GCG ATG CGC ATG GCC TTC AAC CCC GTC CAG GGC

T   A   D   L   M   K   L   A   M   V   K   L   F   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC AGG CTG GAG

E   M   G   A   R   M   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTT CAG GTC CAC GAC GAG CTG GTC CTC GAG GCC

P   K   E   R   A   E   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCC GAG GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC TGG
```

FIGURE 1700 (CONT.)

```
L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGG CAT CAT CAT CAT

H   H   //
CAT CAT //

M   V   K   V   K   F   K   Y   K   G   E   E   K   E   V   D   T   S
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GTA GAC ACT TCA

K   I   K   K   V   W   R   V   G   K   M   V   S   F   T   Y   D   D
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC

N   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

L   D   M   L   A   R   A   E   R   E   K   K   //  *
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG
```

Figure 17PP

Pfu DNA Polymerase (WT)-Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69)

//

cctggtcct gggtccacat atatgttctt actcgcctt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat

caactctaca cctccccat tttctctctt atgagattt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

FIGURE 17PP (CONT.)

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtagag aaggttgaga aaagtttct cggcaagcct attaccgtgt ggaaacttta

tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

aataccaatg gaggggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat

agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact

tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga

tatgacggct gtagaagtca agggaagaat acattcgac ttgtatcatg taataacaag

gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc

aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga

gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt

ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag

gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga

agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac

FIGURE 17PP (CONT.)

```
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agtttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca ataggcaat tcattgagaa ccaggttctt ccagcggtac ttaggatatt
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
```

FIGURE 17PP (CONT.)

```
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta

tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct

acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccgggagt tttgtattgc tctagccaag gttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag cccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg   //
```

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA GAA TTA
```

FIGURE 17PP (CONT.)

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 17QQ

<u>Sac7d - Pfu DNA Polymerase (WT) fusion protein</u>

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA GAC
   TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
//
cctggtcct gggtccacat atatgttctt actcgcctt atgaagaatc cccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat

caactctaca cctcccctat ttctctctt atgagatttt taagtatagt tatagagaag

gtttatact ccaaactgag ttagtagata tgtgggggagc ataatgatt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt

taagatagag catgatagaa ctttagacc atacatttac gctcttctca gggatgattc

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt

tgatgtgagag aaggttgaga aaagttct cggcaagcct attaccgtgt ggaaacttta

tttggaacat cccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct

aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
```

FIGURE 17QQ (CONT.)

```
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggggaaga aagtacatcg agtttagtatg
```

FIGURE 17QQ (CONT.)

```
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca ataggggcaat tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaaatccta gaaaagcgat agatatcaac tttattctt
tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttattta
tgggtaatta aaaaaccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt
ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct
cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct
tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt
```

FIGURE 17QQ (CONT.)

tttgctccaa gcagagccgc tccaatggat aacacccctg ttccgcacc caagtccgct

acaattttt cctgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccgggagt tttgtattgc tctagccaag gttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gttttaagt atgaaatttt tcttccatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgttcttgg // TGA

Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 27)
Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

FIGURE 17RR (CONT.)

```
ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
```

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT  120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA  180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT  240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT  300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC  360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC  420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT  480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC  540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG  600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG  660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAAGAATACA CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGTCAAGG TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAGAAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
```

FIGURE 17RR (CONT.)

```
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
// TGA
```

Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) –Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGAA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGAATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
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FIGURE 17SS (CONT.)

```
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGAGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
```

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG ATG TTA GCA AGA GCA AGA GAG GAG AAG AAA // TGA

Figure 17TT

<u>PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein</u>

Nucleotide sequence (SEQ ID NO: 29)   // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 30)   // Nucleotide sequence (SEQ ID NO: 69)

FIGURE 17TT (CONT.)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT  120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA  180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT  240
ACCGTGTGGA AACTTTATTT GGAACATCCC CCACTATTAG AGAAAAAGTT  300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC  360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC  420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT  480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC  540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG  600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG  660
AAAAGGGCAG AAAAACTTGG GATTAAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGACACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AAGGTCCTCAC 2040
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FIGURE 17TT (CONT.)

```
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
```

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA GCA GAA AGA GAG GAG AAG AAA // TGA
```

Figure 17UU

<u>**PFU DNA POLYMERASE (G387P/V93R OR E)-Sac7d fusion protein**</u>

Nucleotide sequence (SEQ ID NO: 29) //Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 30) //Nucleotide sequence (SEQ ID NO: 69)

```
G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACACTCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
```

FIGURE 17UU (CONT.)

```
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGT TGGATTCGTT AAAGAGCCAG AAAAGGGGGT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT TAAGGAGTGT GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTCG GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AACAAGACCA TTACATGAGT ATAAGGCGAT ACCAGAGAAG 1980
CTCGCCAATA TATGAGCAGA TCAAAGAAAC AGCTGCTAAA TAAAGCCAGG AAGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT TACTTAGAGG CGATGGTCCA ATTAGCAATA AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGACGCA GAATATTACA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GGGATTTGGA TACAGAAAGG GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TTCCTGGCTT AACATTAAAA AATCC // 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // 2328
```

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA AGA GCA GAA AGA GAG GAG AAG AAA // TGA
```

Figure 17VV

SAC7D-PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein

Nucleotide sequence (SEQ ID NO: 69)   // Nucleotide sequence (SEQ ID NO: 31)
Nucleotide sequence (SEQ ID NO: 69)   // Nucleotide sequence (SEQ ID NO: 32)

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA GCA GCA AGA AGA GAG GAG AAG AAG AAA //
```

GCNATAGCNA (underlined portion)

```
//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
```

FIGURE 17VV (CONT.)

```
CTCAGGGAGA GCTACACAGTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAGAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT TTCCTGGCTT AACATTAAAA AATCC // 2328
```

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
```

FIGURE 17WW (CONT.)

```
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC  360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC  420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA  480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC  540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG  600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA  660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG  720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC  780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA  840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA  900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC  960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC  1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG  1080
GCCTATGAGA GGAATGAGCT GGCCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA  1140
CGGCAGAGCT ATGAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA  1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG  1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC  1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG  1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT  1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA  1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC  1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC  1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT  1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG  1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA  1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTAGCGCGA GATAGCGAAA  1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG  1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG  1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT  2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC  2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACCAGG CGATACCGTT CGACGAGTTC  2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC  2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG  2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT  2325
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
   AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
   AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
   TTA GAC ATG TTA GCA AGA GCA GAA GAA GAG AAG AAA // TGA
```

Figure 17XX

Sac7d – KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //
```

```
//ATGGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAAACTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA AGTCGCCCGC TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
```

FIGURE 17XX (CONT.)

```
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTGCCAC AATACCTGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA GGCCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC CCGAAGGGAA CT //TAG 2325
```

Figure 17YY

<u>Sac7d-Vent DNA POLYMERASE FUSION PROTEIN</u>

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG GCA ACA GCA GAA AGA AGA GAG AAG AAG AAA //

ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGAGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
```

FIGURE 17YY (CONT.)

```
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA  300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT  360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT  420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT  480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT  540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA  600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA  660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA  720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT  780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT  840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA  900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA  960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC CAAAGGGAGC GCAAGAGGGA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA AAACCAAGTT TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
```

Figure 17ZZ

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG    60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT   120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA   180
AAAACTGTGA GAGTGCTCGA TGCCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT   240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA   300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT   360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT   420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT   480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT   540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA   600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAAATT TTGATTTGCC GTATCTCATA   660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA   720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGTGAAA TCAAGGGTAG AATCCACTTT   780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT   840
TATGAAGCAG TTTTAGGAAA AACCAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA   900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA   960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT  1020
CAAGGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA  1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA  1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG  1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC  1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA  1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT  1380
```

FIGURE 17ZZ (CONT.)

```
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GG 2325 //
```

```
// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA GCA GAA AGA GAG GAG AAG AAA // TGA
```

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37)   // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 38)   // Nucleotide sequence (SEQ ID NO: 69)

FIGURE 17AAA (CONT.)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGTAC   300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCCGTG GAGATAAAGG GAAGGATACA CTTTGACCTC   780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC   960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC  1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG  1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG  1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG  1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA  1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC  1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT  1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC  1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA  1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA  1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA  1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC  1740
GAGGCTTCTT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG  1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC  1860
AAAGAAACCC AAGCAAAAGT CCTAAAGAGC ATGGCAACGT ATGGCAACGT TGAGGAGGCA  1920
GTAAAGATAG TTAAGGAGGT CTTCACGAGT ACAAGGCTAT ACGAAATACC TCCAGAAAAG  1980
CTAGTTATTT ACGAGCAGAT CACGAGCGCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC  2040
GTTGCCGTGG CAAAAAGGTT GGAGTAAAGG GGAGTAAAGG TGAGGTAAAG CATGGTGATA  2100
GGGTACATAG TGCTGAGGGG AGACGGGGCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG  2160
```

FIGURE 17AAA (CONT.)

TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG 2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // 2328

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TGA

Figure 17BBB

<u>Sac7d - Deep Vent DNA polymerase fusion protein</u>

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA GCA AGA AGA GAA GAG AAG AAA //

//ATGGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG   60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGGTAC   300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC   780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC   960
GAGCTCGGTA GGGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC   1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG   1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG   1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG   1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA   1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC   1320

FIGURE 17BBB (CONT.)

```
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGAGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT  1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC  1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA  1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA  1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA  1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC  1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG  1800
GAAGGAAGA TAATCACTAG GGGGCTTGAA ATAGTTCAGA GGGACTGGAG CGAAATAGCC  1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA  1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG  1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC  2040
GTTGCCGTGG CAAAAAAGGTT AGCCGCCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA  2100
GGGTACACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG  2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT  2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG  2280
ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA              2328
```

Figure 17CCC

JDF-3 - Sac7d fusion protein

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69)
Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATCTCCTTGACGTTGATTACATCACCGAGAATGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGCGCTTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCCGGGAGGAGCACGACGGGGTCGTCGTTAAGCGCGCGGAAGGTGAAGAAAAAGTTCCTCGG
CAGGTTCTGTGAGGTCTGGGTCCTTACTTCACGGCGTACTTCACGACAAGGCCTAAACTCAGTCCTTCGAGGAGATCCGCAAATAACTCATGTCCTTCGAGAGATCCTAC
TTCGGCAAGGCCGATTCATGATGATAAGCTACGCCGAGAAGCTACGCCGTGATAATCCGGACGTGCTGATAACATACAACGGGCGACAACTTCGACTTCCTGCCCTACCTGTGAAAAAGCTCGTGTGAGGAAGCTTGGCGTGAGCTTT
GCGCTTCTTGAGGGTCGTTAAGGAGCGGCGAGCCGAAGATACAGCGCGGCGGTTTCGGCAAGCCCAAGGAGAGATAGCCACCGCGCCTGGGAGACCGGGCGAGGGCTTGAGAG
```

FIGURE 17CCC (CONT.)

GGTCGCGCGCTACTGCACTCGATGGAGGACGCGGAGGGTTACTCACTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCCTCCTAAGAAGGCCTACGAGAGGAACGAACTCGCTCCGACGAACTGCTCCACAAGCGTCTCGCCAGATAC
ACgccGGTGGCTACGTCAAGGAGGCCGGAGCGGGGACTGTGGGACAATATATCGTTATCTAGACTTTCGTAGTCTCTAC[CCT]CAATCATAATCACCCACAACGTCTCGCCAGATAC
GCTCAACCGTGTAGGAGCTACGACGTTGCCCCGAGTCGGTCAAGTTCTGCAAGGAATCTCCGCTTCATTCCGAGCCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATTCTCGATTACAGGCAACGC[GC]ATCAAGATTCGCCAACAGCTACTACGGCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCACGGTAGCGCCACCATTCCTGAGCGGACGCGTTACGGCAGAAATGGTCATCAGAGAGCTTGAGGAAAAAGTTCGGTTTTAAAGTCCT
CTATGCAGACAGACAGACGGTCTCCATGCCACCATTCCTGAGCGGCTTCTACGTGCAGGGCTTCTCAGGGGCGGAGGCAGGGAAGAGACGCAAGAACAGTCAAGAAAAAGCAATGAGTTCTTAAACTATATCAATCCAAACTGCCCGGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTGCAGGCCTTCAGGGGCGGAGGGTTTGGAGGCGCACGGTGACGTTGAGGCGCACGGTGAAGAGCAGAATTGTCAGGGAAGTTGTCAGGAAGTGCTGAGCAA
ACTGGAGCGAGATAGCGAAGGAGACGCAGGGAGGTTATCACGAGCAGATAACGCGCAGGCCACCGGCCCGCCACGTAGCGAAGCGTTTGGCCGCAGAGGT
GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCGAGCAGATAACGCGCAGGCTCAAGGCGCTCCGGAAGGGATAGGCGACGTTCGACGAGTTGACCGAGAGGT
GTTAAAATCCGGCCGGAACTGTGATAAGCTACATCGTTCTGCGGCAGTTGAGAGAATCCTGAGAGAGAAGACCTGCGCTACCGAGAAGACGAGGCAGGTGTCGGCGC
GTGGCTGAAGCCGAAGGGGGAAGGGGAAGAGAAG//

//ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA AGA GCA GAA GAG AGA GAC ACT TCA // TAG

Figure 17DDD

<u>**Sac7d - JDF-3 fusion protein**</u>

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)
Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AAG, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA
AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC
AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA
TTA GAC ATG TTA GCA AGA AGA GCA GAA GAG AGA GAG AAG AAG AAA //

FIGURE 17DDD (CONT.)

//ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTT
CTACGCGCTCCTCCTCAGGGACGACGACTCTGCCATCGAAGAGAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAAGGTGAAGAAAAGTTCCTC
GGCAGGTCTCGTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGGCACAAAAATAAGGAAGCACACCCGCGGTCATCGAGTACGACATAC
CCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTCGAGATCGAGACGCTCTACCACGAGGAGGAGAAGAGTTTGG
AACCGGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCGTGCTGATAACATACAACGGCGAGTGCCGACGTGCTGTGAGGTTGTCTCCACCGAGAAGGAGATGATT
AAGGCTTCTTGAGGGTCGTTAAGGAGGGAGACGGAGCCGAAGATACAGCGCCAGGTTTGCGGTCGAGGTACACTTGACCTTTATCCAGTCATAAGGCGCACCAT
TTACCCTCGGGAGGGAGGGACGGGAGCGAGCCGAAGATACAGCGCCATGGGGGTTTCGGCAAGCCCAAGGAGAAGGTCTACCGCGAGAGATAGCCACGGCCTCTGGGACGTTT
AAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTACTTGGCAGGGTTCTTCCCGATGGAGGCCCAGCTTCTCATGGCCCAAGGCCTCTGGGACGTTT
AGGGTCGCGCTACTCGATGGAGACGCGAGGGTTACCTCGAGTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTCTCATGGCCCAAGAGCTGGCGAGGAGGGGGG
CCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCCCAACAGCCCGACGAGAGGAGCTGGCGAGGAGGAGGGGGG
CTACgcCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGGACAATATCGTGTATCTGAGTCTCTAC[CCT]CAATCATAATCACCCACAACGTCTCGCCAGAT
ACGCTCAACCGCGAGGGGTGTGAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTTCTGCAAGGACTTCCCGAGCTTCATTCGGAAACCTGCTGGAGGAAA
GGCAGAAGATAAAGAGCAAGAATGGTACTGCAGGGAGTGCGCCGAGACGCGTTACGGCAACGC[GCC]ATCAAGATTCTGCCAACAGCTACTACGGCTACTACGG
CTATGCCAGGGCAAGACACAGACGGTCTCCACCATTCCTCGAGGCGAGAGCGTTGAGGAAAAGTTCGGTTTTAAAGTC
CTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGAGGCGAGAGCGTTAAATCAATCCAAACTGCCCGGCCTTC
TCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAGAAAGTACGGCAAGATAACCAGTGTGGGCTTGAGATAGTCAGGCG
CGACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGGTTTGGAGGCGATACTCAGGCGGTTGAAGGCGTCAGAATTGTCAGGGAAGCTGAGC
AAGTACGAGGTTCCGCCGAGAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCCGGCGTTCGACCCGACGCAAGTACGA
GTGTTAAATCGGCCCGGCCGCGAACTGTATAGCTACATCGTTCTGAAGGGCGACAGGGCGATTCCTTCGACGAGTTCGACCCGCTACCAGAAGACCTGCGCTACCGGCCTTCGGCTACACCG
TGCGGACTACTACATCGAGAACCAGGTTCTGCCGCAGTTGAGAGAATCCTCAGGGCCTTCGGGCTACACCGGCGTACTACATCGAGAACCAGGAAGAGACGAGCGAGGCAGGTCGGGCTTGGC
GCGTGGCTGAAGCCCGAAGGGGGAAGAAGAAGTGA

Figure 17EEE

Synthetic Sso7d gene:

Nucleotide sequence (SEQ ID NO: 71)
Amino acid sequence (SEQ ID NO: 72)

```
 A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

 I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

 G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

 L   Q   M   L   E   K   Q   K   K
CTG CAG ATG CTG GAG AAG CAG AAA AAG
```

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)
Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66)

```
//  A   T   V   K   F   K   Y   K   G   E   E   K   E   V   D   I   S   K
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

 I   K   K   V   W   R   V   G   K   M   I   S   F   T   Y   D   E   G
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

 G   G   K   T   G   R   G   A   V   S   E   K   D   A   P   K   E   L
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

 L   Q   M   L   E   K   Q   K   K   //   G   G   G
CTG CAG ATG CTG GAG AAG CAG AAA AAG  //  GGC GGC GGT
```

FIGURE 17FFF (CONT.)

```
V    T    S    G    M    L    P    L    F    E    P    K    G    R    V    L    L    V
GTC  ACT  AGT  GGG  ATG  CTG  CCC  CTC  TTT  GAG  CCC  AAG  GGC  CGG  GTC  CTC  CTG  GTG

D    G    H    H    L    A    Y    R    T    F    H    A    L    K    G    L    T    T
GAC  GGC  CAC  CAC  CTG  GCC  TAC  CGC  ACC  TTC  CAC  GCC  CTG  AAG  GGC  CTC  ACC  ACC

S    R    G    E    P    V    Q    A    V    Y    G    F    A    K    S    L    L    K
AGC  CGG  GGG  GAG  CCG  GTG  CAG  GCG  GTC  TAC  GGC  TTC  GCC  AAG  AGC  CTC  CTC  AAG

A    L    K    E    D    G    D    A    V    I    V    F    D    A    K    A    A    P
GCC  CTC  AAG  GAG  GAC  GGG  GAC  GCG  GTG  ATC  GTG  TTT  GAC  GCC  AAG  GCC  GCC  CCC

S    F    R    H    E    A    Y    G    Y    G    K    Y    A    R    A    P    T    P
TCC  TTC  CGC  CAC  GAG  GCC  TAC  GGG  TAC  GGG  AAG  TAC  GCG  CGG  GCC  CCC  ACG  CCA

E    D    F    P    R    Q    L    A    L    I    K    E    L    V    D    L    L    G
GAG  GAC  TTT  CCC  CGG  CAA  CTC  GCC  CTC  ATC  AAG  GAG  CTG  GTG  GAC  CTC  CTG  GGG

L    A    R    L    E    V    P    G    Y    P    G    E    A    D    V    L    S    L
CTG  GCG  CGC  CTC  GAG  GTC  CCG  GGC  TAC  CCG  GGC  GAG  GCC  GAC  GTC  CTG  AGC  CTG

A    K    A    E    K    A    E    G    Y    E    G    V    R    I    T    A    D    K
GCC  AAG  GCG  GAA  AAG  GCC  GAG  GGC  TAC  GAG  GGC  GTG  CGC  ATC  ACC  GCC  GAC  AAA

D    L    Y    Q    L    S    D    R    I    H    V    H    L    P    E    G    Y
GAC  CTT  TAC  CAG  CTT  TCC  GAC  CGC  ATC  CAC  GTC  CAC  CTC  CCC  GAG  GGG  TAC

L    I    T    P    A    W    L    E    K    Y    G    L    R    P    D    Q    W
CTC  ATC  ACC  CCG  GCC  TGG  CTT  GAA  AAG  TAC  GGC  CTG  AGG  CCC  GAC  CAG  TGG

A    D    Y    R    A    L    T    G    D    E    S    D    N    P    G    V    K
GCC  GAC  TAC  CGG  GCC  CTG  ACC  GGG  GAC  GAG  TCC  GAC  AAC  CCC  GGG  GTC  AAG

G    I    G    E    K    T    A    R    K    L    L    E    W    G    S    L    E
GGC  ATC  GGG  GAG  AAG  ACG  GCG  AGG  AAG  CTT  CTG  GAG  TGG  GGG  AGC  CTG  GAA

A    L    L    K    N    L    D    R    L    K    P    A    I    R    E    K    I    L
GCC  CTC  CTG  AAG  AAC  CTG  GAC  CGG  CTG  AAG  CCC  GCC  ATC  CGG  GAG  AAG  ATC  CTG

A    H    M    D    D    L    K    L    S    W    D    L    A    K    V    R    T    D
```

FIGURE 17FFF (CONT.)

```
A   H   M   D   D   L   K   L   S   W   D   L   A   K   V   R   T   D
GCC CAC ATG GAC GAT CTG AAG CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC

L   P   L   E   V   D   F   A   K   R   R   E   P   D   R   E   R   L
CTG CCC CTG GAG GTG GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT

R   A   F   L   E   R   L   E   F   G   H   E   F   G   L
AGG GCC TTT CTG GAG AGG CTT GAG TTT GGC CAC GAG TTC GGC CTT

L   E   S   P   K   A   L   E   E   W   P   P   P   E   G   A
CTG GAA AGC CCC AAG GCC CTG GAG GAG TGG CCC CCG CCG GAA GGG GCC

F   V   G   F   V   L   S   R   K   E   M   W   P   D   L   L   A
TTC GTG GGC TTT GTG CTT TCC CGC AAG GAG ATG TGG CCC GAT CTT CTG GCC

L   A   A   A   R   V   R   H   L   R   A   P   E   P   Y   K   A
CTG GCC GCC GCC CGG GTC CGG CAC CTT CGG GCC CCC GAG CCC TAT AAA GCC

L   R   D   L   K   A   L   L   K   D   D   L   S   V   L
CTC AGG GAC CTG AAG GCG CTT CTC AAA GAC GAC CTG AGC GTT CTG

A   L   R   E   G   L   G   P   D   D   M   L   L   A
GCC CTG AGG GAA GGC CTT GGC CCC GAC GAC ATG CTC CTC GCC

Y   L   D   P   S   N   T   P   E   R   R   Y   G
TAC CTC GAC CCT TCC AAC ACC CCC GAG CGG CGC TAC GGC

G   E   W   T   E   E   E   G   E   A   L   S   E   R   L   F
GGG GAG TGG ACG GAG GAG GAG GGG GAG GCC CTT TCC GAG AGG CTC TTC

A   N   L   W   L   L   W   L   Y   R
GCC AAC CTG TGG CTT CTC TGG CTT TAC CGG

E   E   R   P   L   S   A   V   H   M   A   T   G   V
GAG GAG AGG CCC CTT TCC GCT GTC CAC ATG GCC ACG GGG GTG

E   V   D   V   Y   A   A   V   A   E   E   I
GAG GTG GAC GTG TAT GCC GCC GTG GCC GAG GAG ATC

R   L   D   V   A   Y   L   R   A   L   S   R   R   R
CGC CTG GAC GTG GCC TAT CTC AGG GCC TTG TCC CGC AGG CGG

A   R   L   E   V   F   R   A   L   A   H   P   F   N   L   N
GCC CGC CTC GAG GTC TTC CGC GCC CTG GCC CAC CCC TTC AAC CTC AAC
```

FIGURE 17FFF (CONT.)

```
S     R     D     Q     L     E     R     V     L     F     D     E     L     G     L     P     A     I
TCC   CGG   GAC   CAG   CTG   GAA   AGG   GTC   CTC   TTT   GAC   GAG   CTA   GGG   CTT   CCC   GCC   ATC

G     K     T     E     K     T     G     K     R     S     T     S     A     A     V     L     E     A
GGC   AAG   ACG   GAG   AAG   ACC   GGC   AAG   CGC   TCC   ACC   AGC   GCC   GCC   GTC   CTG   GAG   GCC

L     R     E     A     H     P     I     V     E     K     I     L     Q     Y     R     E     L     T
CTC   CGC   GAG   GCC   CAC   CCC   ATC   GTG   GAG   AAG   ATC   CTG   CAG   TAC   CGG   GAG   CTC   ACC

K     L     K     S     T     Y     I     D     P     L     P     D     L     I     H     P     R     T
AAG   CTG   AAG   AGC   ACC   TAC   ATT   GAC   CCC   TTG   CCG   GAC   CTC   ATC   CAC   CCC   AGG   ACG

G     R     L     H     T     R     F     N     Q     T     A     T     A     T     G     R     L     S
GGC   CGC   CTC   CAC   ACC   CGC   TTC   AAC   CAG   ACG   GCC   ACG   GCC   ACG   GGC   AGG   CTA   AGT

S     S     D     P     N     L     Q     N     I     P     V     R     T     P     L     G     Q     R
AGC   TCC   GAT   CCC   AAC   CTC   CAG   AAC   ATC   CCC   GTC   CGC   ACC   CCG   CTT   GGG   CAG   AGG

I     R     R     A     F     I     A     E     G     W     L     L     V     A     L     D     Y
ATC   CGC   CGG   GCC   TTC   ATC   GCC   GAG   GGG   TGG   CAC   CTA   GTG   GCC   CTG   GAC   TAT

S     Q     I     E     L     R     V     L     A     H     L     S     G     D     E     N     L     I
AGC   CAG   ATA   GAG   CTC   AGG   GTG   CTG   GCC   CAC   CTC   TCC   GGC   GAC   GAG   AAC   CTG   ATC

R     V     F     Q     E     G     R     D     I     H     T     E     T     A     S     W     M     F
CGG   GTC   TTC   CAG   GAG   GGG   CGG   GAC   ATC   CAC   ACG   GAG   ACC   GCC   AGC   TGG   ATG   TTC

G     V     P     R     E     A     V     D     P     L     M     R     R     A     A     K     T     I
GGC   GTC   CCC   CGG   GAG   GCC   GTG   GAC   CCC   CTG   ATG   CGC   CGG   GCG   GCC   AAG   ACC   ATC

N     F     G     V     L     Y     L     G     M     S     A     H     R     L     R     S     Q     E     L     A
AAC   TTC   GGG   GTC   CTC   TAC   CTC   GGC   ATG   TCG   GCC   CAC   CGC   CTC   CGC   TCC   CAG   GAG   CTA   GCC

I     P     Y     E     E     A     Q     F     I     E     K     T     L     E     R     Y     Q     S     F     P
ATC   CCT   TAC   GAG   GAG   GCC   CAG   TTC   ATT   GAG   AAG   ACC   CTG   GAG   CGC   TAC   CAG   AGC   TTC   CCC

K     V     R     A     I     W     E     K     T     L     E     G     R     R     R     R     G     Y
AAG   GTG   CGG   GCC   ATT   TGG   GAG   AAG   ACC   CTG   GAG   GGC   AGG   CGG   AGG   CGG   GGG   TAC

V     E     T     L     F     G     R     R     R     Y     V     P     D     L     E     A     R     V
GTG   GAG   ACC   CTC   TTC   GGC   CGC   CGC   CGC   TAC   GTG   CCA   GAC   CTA   GAG   GCC   CGG   GTG
```

FIGURE 17FFF (CONT.)

```
K   S   V   R   E   A   A   E   R   M   A   F   N   M   P   V   Q   G
AAG AGC GTG CGG GAG GCG GCC GAG CGC ATG GCC TTC AAC ATG CCC GTC CAG GGC

T   A   D   L   M   K   L   A   M   V   K   L   F   P   P   R   L   E
ACC GCC GAC CTC ATG AAG CTG GCT ATG GTG AAG CTC TTC CCC     AGG CTG GAG

E   M   G   A   R   M   L   Q   V   H   D   E   L   V   L   E   A
GAA ATG GGG GCC AGG ATG CTC CTT CAG GTC CAC GAC GAG CTC GTC CTC GAG GCC

P   K   E   R   A   E   A   V   A   R   L   A   K   E   V   M   E   G
CCA AAA GAG AGG GCG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG GGG

V   Y   P   L   A   V   P   L   E   V   G   I   G   E   D   W
GTG TAT CCC CTG GCC GTG CCC CTG GAG GTG GGG ATA GGG GAG GAG GAC TGG

L   S   A   K   E   G   I   D   G   R   G   G   G   H   H   H
CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT CAT

H   H   *
CAT CAT TAA
```

Figure 17GGG

Pfu DNA Polymerase (WT)-Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

```
//
cctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc
tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttattctat
caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag
gtttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga
```

FIGURE 17GGG (CONT.)

```
ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt
taagatagag catgatagaa ctttagacc atacatttac gctcttctca gggatgattc
aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt
tgatgtagag aaggttgaga aaagtttct cggcaagcct attaccgtgt ggaaacttta
tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt
tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct
aataccaatg gaggggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta
tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa
tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag
cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat
agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact
tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga
tatgacggct gtagaagtca agggaagaat acattcgac ttgtatcatg taataacaag
gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc
aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga
gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt
ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgttcaag
gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aagaaaacga
agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac
aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt
tagagccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct
```

FIGURE 17GGG (CONT.)

```
tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat
cctggtttt  ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac
aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc
gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta
ctgtaaggag tgtgctgaga gcgttactgc ctgggaaga  aagtacatcg agttagtatg
gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta
tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa
atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag
gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac
tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag
agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga
agtaatacaa aagcttgcca attatgaaat tccaccagaa aagctcgcaa tatatgagca
gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa
actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag
aggcgatggt ccaattagca ataggcaat  tctagctgag gaatacgatc ccaaaaagca
caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt
ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct
aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac tttattctt
tctaacctttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta
tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc
```

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FIGURE 17GGG (CONT.)

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct

acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct

ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt

taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta

gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga

aagattgaga tgtttcttgg //

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC

GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

CTG CAG ATG CTG GAG AAG CAG AAA AAG   // TGA

Figure 17HHHH

PFU DNA POLYMERASE (V93 R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA  60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT  120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGAA  180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG AGTTTCTCGG CAAGCCTATT  240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC AGAAAAAGTT  300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA AAAGAGATAC  360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC  420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT  480
AGTTATGCAG ATGAAAAATGA AGCAAAGGTG ATTACTTGGA AAAAACATAGA TCTTCCATAC  540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAAGAGAT TTCTCAGGAT TATCAGGGAG  600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG  660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA AGTTCCAATGGAAGATGCAAA AGGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGGAA TACTCGATGG CAAGATTAGT TGGACAACCT  1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA  1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG  1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC  1200
ATATATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT  1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC  1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA  1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT  1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT  1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG  1560
TACATCGAGT TAGTATGGAA GGGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT  1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG  1680
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FIGURE 17HHH (CONT.)

```
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGGA ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACACAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG CAG AAA AAG // TGA
```

Figure 17III

PFU DNA POLYMERASE (G387P/V93R OR E) -Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 29)   // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 30)   // Nucleotide sequence (SEQ ID NO: 71)

```
G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGAA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
```

FIGURE 17III (CONT.)

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ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAGGCGAT TAAGGAGTGT GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGACTCG GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //              2328
```

```
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GAG GGC
   GGT GGC AAG GGC GGC CGT GGT GTA AGC GTA AAG GAC GCG CCG AAG GAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG   // TGA
```

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E)-Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17JJJ (CONT.)

```
D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA   60
AAAGAGAACG GAAAATTTAA GATAGAGCAT TTAGACCATA CATTACGCT              120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA  180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG AGTTTCTCGG CAAGCCTATT            240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG AGAAAAAGTT  300
AGAGAACATC CAGCAGTTGT GGACATCTTC TTCCATTTGC AAAGAGATAC            360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC  420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT  480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC  540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG TTCTCAGGAT TATCAGGGAG            600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG  660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAAGTCAAGG CGAGCCCAAG  720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG  780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA  840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA  900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT  960
GAACTCGGGA AAGAATTCCT TCCAATGAAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGT TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AGCTCCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGTCCTCAC  2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGTGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
```

FIGURE 17JJJ (CONT.)

GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //   2328

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG GCC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG   //   TGA

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein

Nucleotide sequence (SEQ ID NO: 33)   // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 34)   // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAAACGTGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGTCTGG AATAAACTTC GCCCTCGGAA GGGATGAAG CGAGCCGAAG 720
ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780
TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG GAGACCTCCT AGAGGAGAGG 1380

FIGURE 17KKK (CONT.)

```
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCCAGA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG CGCTTGAGCT CGAGTACGAG 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGACGCGA GATAGCGAAA 1860
GAGACGCGAGG CGAGGGTTCT CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325
```

// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA

Figure 17LLL

Sso7d - KOD DNA POLYMERASE fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)
Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG CTG GAG AAG CAG AAA AAG //

FIGURE 17LLL (CONT.)

```
//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG   60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC  120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG  180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT  240
GAGGTCTTGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG GGACAAGATA  300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC  360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC  420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA  480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC  540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG  600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG  660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GTTTGCCGTC GAAGTGAAGG GACGGATACA  720
ATTCAGAGGA TGGGCGACAG TCTCCCGCTC CAGCACTGGC AAGCCCGATG CTTCGATCTC  780
TATCCTGTGA TAAGACGGAC GATAAACCTG CTATGTAAAA CCTGTACCCC TCAATCATCA  840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA  900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC  960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG GAGCCCGAGA GAGGGTTGTG GGAGAACATA CGTCTCGCCG 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGGCCACCGC 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACCAGT AGAGGAGAGG 1320
TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG AGCCTGCTTG GCTCCTCGAT 1380
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA AACAGCTACT CGGCTATGCA 1440
TACAGGCAGA GGGCCATCAA GATCCTGTGCA GGAGTGTGCA CGGCCTGGGG AAGGGAGTAC 1500
AGGGCCGCGT GGTACTGCAA GGAGTGTGCA GATAGAGGAA GTGACGTCGA CTACAGCGAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AGTACGGCTG TTAAGGTAAT AAAGAAGGCT 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA CGAGTACGAG 1680
ATGGAGTTCC TCAAGTATAT CAACGCCAAA CTTCCGGGCG AAGAAGAAGT AGACGAGGAA 1740
GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT GATAGCGAAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATACCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
AGGATAGTCA AAGAAGTTAC CGAAAAGCTG AGCAAGTACG AGGTTCCGCC GGAGAAGCTG 1980
GTGATCCACG AGCAGATAAC GAGGGATTTA AGGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA CGACGCCGAG ACTGGAGCGA CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT //TAG 2325
```

Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)
Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
  ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
  GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
  CTG CAG ATG CTG GAG AAG CAG AAA AAG   //
```

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG  60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGAAGTT  240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT TTTATTCCCT GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
```

FIGURE 17MMM (CONT.)

```
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG ATAGAGGAAA AAAGCGGTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACACA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGGAG CGGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAAATACG ATCCTAGAAA ACACCAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
```

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN

Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGAGAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGACXXXC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
```

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FIGURE 17NNN (CONT.)

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TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGGGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACCAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAAACCGG CTTAGATGCA TGGCTCTCAAGA GG 2325 //
```

```
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
GGT GGC AAG ACC GGC CGT GGT GGC GTA AGC GAC AAG GAC GCG CCG AAG GAG CTG
CTG CAG ATG CTG GAG AAG CAG AAA AAG // TGA
```

Figure 17OOO

Deep Vent- Ssod7 DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 37)   // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 38)   // Nucleotide sequence (SEQ ID NO: 71)

FIGURE 17000 (CONT.)

```
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC TTAGACCTTA CATTTACGCT              120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT   240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA   300
AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC   360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC   540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG   600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCCGTG GAGATAAAGG GAAGGATACA CTTTGACCTC   780
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG   840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG   900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC   960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC  1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG  1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AGCCGGATG AGAGGGAGTA CGAGAGAAGG   1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG  1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA  1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC  1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA  1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT   1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC  1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA  1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA  1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA  1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC  1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG  1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC  1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA  1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG  1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGTCCGCAC   2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA  2100
GGGTACACAG TGCTGAGGGG AGACGGGCCA ATAAGCAGGA GGGCTATCCT TGCAGAGGAG  2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT  2220
GCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAACAGA CAGTCTTAC GGCATGGCTT AACATCAAGA AGAAG                   2328
```

FIGURE 17000 (CONT.)

```
// GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
   ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
   GGT GGC AAG GCC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
   CTG CAG ATG AAG CTG GAG AAG CAG CAG AAA AAG // TGA
```

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37)
Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 38)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
  ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC
  GGT GGC AAG GCC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG
  CTG CAG ATG AAG CTG GAG AAG CAG CAG AAA AAG  //
```

```
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG    60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT   120
CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG   180
AAGATAGTGA GAATTATAGA TGCCGAAAAG AGTTCCTGGG GAGGCCGATT             240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA   300
AGGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC  360
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT   420
GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA   480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAAACGTGG AAAAAGATCGA TCTCCCGTAC  540
GTCGAGGTAG TTTCCAGCGA GAGGGAGATG TCCTCAAGGT GATAAGGGAG             600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT   660
AGAGGGCCG  AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG   720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC   780
```

FIGURE 17PPP (CONT.)

```
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACACATACA CCCTCGAGGC AGTTTATGAG    840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG    900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC    960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC   1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG   1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA CGAGAGAAGG   1140
CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAAGGCT CTGGGAGGGG   1200
TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA   1260
CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC   1320
AAGTTCTGCA AGGACTTCCC GGGGTTTATC TCCAAGAGGT ATTGGATGAA GAAGATGCTT   1380
AGGCAAGAAA TAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT   1440
GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC   1500
GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA   1560
TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA   1620
GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA   1680
GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC   1740
GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG   1800
GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC   1860
AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA   1920
GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG   1980
CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC   2040
GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA   2100
GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG   2160
TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAAATCA GGTTTTACCT   2220
GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG   2280
ACTAAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA              2328
```

Figure 17QQQ

<u>JDF-3 – Sso7d fusion protein</u>

Nucleotide sequence (SEQ ID NO: 39)   // Nucleotide sequence (SEQ ID NO: 71)
Nucleotide sequence (SEQ ID NO: 40)   // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ATGATCCTTGACGTTGATTACATCACCGAGAATGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGGCGAGTTCGAGCCCTACTTCT
ACGCGCTCCTCAGGAGACGACTCGTGCCCATCGAAGACGCGGGTCGTGCCGGAGAGGCGGTCAGGGTCGTTAAGGTTAAGCGCGGAGAAGGTGAAGAAAAGTTCCTCGG
CAGGTCTGTGGAGTGTCGGGTCCTCTACTTCACGCACGCAGCGACAAAATAAGGAGCACCCCCGCAATCCGGCAATCCGGACAAAATAAGGAGTACGACACATACCC

FIGURE 17QQQ (CONT.)

```
TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTGGACATCGAGACGCTCTTACCACGAGGGAGAAGAGAGTTTGGAA
CCGGGCCGATTCTGATGATGAATAAGCTACGCGCCGATGAAAGCGAGGCGAGGCCGGCCGTGATAACCTGGAAGAAGATCGACCTTCCTTACGTTGAGGTTGTCTCCACCGAGAAGAGATGATTAA
GCGCTTCTTGAGGGTCGTTAAGGAGGACGCCGAAGCGAGCCGAGATACAGCAGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCAGTCATAAGGCGCACCATAA
ACCCTCGGGAGGGACGGGACGCGAGCCGAAGATACAGCAGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCAGTCATAAGGCGGCTTGAGAG
ACCTCCGACCTACACCCTTGAGGCTGTATACGAGGGGTTACGCGAGCTTGGCAGGAGTTCTTCCCGGAGGAGTTGCAGGGCCCAACGAACCTCGGGAGGGACGTTTCC
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAGGCCTACGAGAGGAACGAACTCGCTTCGTGTATCTAGACTTTCGTAGTGTCTACCCTCGCCAGATAC
ACgCCGGTGGCTACGTCAAGGAGCCGGAGCGCGGAGCCGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGTCTCCTCGGAAACCTGCTGGAGGAAAGG
CAGAAGGATAAAGAGGAAGATGAAGCGAACTCTGCCACCTCTGAGGGGTAGTTCGTATCTGAAGGGTTTAAAGTTCTT
ATGCCAGGGCAAGATGTACTGCAGGAGTGCGCCACCATTCCTGGAGGCCGACGTCAAGAAAAAAGGCAAGAGTCAATGGAGTTCTTAAACTATATCAATCCCGGCCTTCTC
CTATGCGAGCCAGACGGTCTCCACCATTCCTGGAGGCCGACGTCAAGAAAAAAGGCAAGAGTCAATGGAGTTCTTAAACTATATCAATCCCGGCCTTCTC
GAACTCGAATACGAGGGCTTCTACGTTCAGGAGGCTTCGCAGGGTTTGGAGGTTTGGAGGCGAGATAACGCGGTCACCGGAAGTGCAAAAGCTGAGCAA
ACTGGAGCGAGATAGCAAGGAGGAAGCTGGTTATCCGACGGAGAGTACTACATCGTTCGCGAAGGGCTCCGAAGGATAGGCGACAGCAGGTCACCGACGT
GTAGAGGTTCCGCCGAGGTTCGCGGCCCCGAACTGTGATAAGCTACATCGTTCGCGCAGTTGACATCGAAGCGACGATGCGCCAGAGGT
GTTAAAATCCGGCCCGGAACCAGTTCTGCCGGGTTCTGCCGGTTCTGCGGTTCTGAGAGAATCCTCAGGGCCTTCAGGGCTCTACCGGCTACCAGAAGACCTGCGCGCTACCAGAAGACGAGGCAGGTTCGGGTTCGCGC
GTGGCTGAAGCCGAAGGGGAAGAGAAG//
```

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC GAC TAC GAC AAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GCG CCG AAG GAG CTG
CTG ATG ATG CTG GAG AAG CAG AAA AAG            // TAG
```

Figure 17RRR

Sso7d - JDF-3 fusion protein

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)
Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
//GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC GAC TAC GAC AAG GGC
GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GCG CCG AAG GAG CTG
CTG ATG ATG CTG GAG AAG CAG AAA AAG            //
```

FIGURE 17RRR (CONT.)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT
ACGCGGCTCCTCAGGGACGACTCTGCCATCGAAGAGATAACCGCGGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGGAGAAGTGAAGAAAAAGTTCCTCGG
CAGGTCTGTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGAC**XXX**CCGGCAATCCGGTCATCGAAGAGCTTAAACTCATGTCCTTC[GAC]ATC[GAG]ACGCTCTACCAGGGGAGAAGAGTTTGGAA
TTCGGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTGGAGAAGCGCGTGATAACAAGAGGCGCGACAACTTCGCCTACCTGCCTACTTCGGCCTTCCACCGAGGAGATGATTAA
CCGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGTGATAACATACAACGGCGACAACTTCGCCTACCTGTGTGAAAAAGCGCTGTGTGAGCTTT
ACCTCGGGAGGAGGACGGGAGCGAGCCGAAGATACAGCGCCATGGGGACCAGGTTTCGGTCGAGGTGACCCTTATCCAGTCATAAGGCGCACCATAA
ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTCGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTTCCAGGCTCTCATCGGCGAGTTTCC
GGTCGCGCTACTCGATGGAGGACGCGAGGGTTACTCACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGCCCAGCTTCATCGGCGCTCAAGAGCTGGCGAGAGGGGGGCT
CGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCCTCCTAAGGAAGGCCTACGAGAGGAACGAACTCGCTCCAAGCCCGAGAGGGAGCTGGCGAGAGAGGGAGGAGGGGCT
ACgCCGGTGGCTACGTCAAGGAGCCGGAGCCGGGAGACGGGGACTGTGGGACAATATCGTGTATCTGAACTTTCGTATCTCTAC[CCT]CAATCATAATCACCCACAACGTCTCGCCAGATAC
GCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCGCCGAGTCGGTCGTCACAAGTTCTGCAAGGACTTCCCGGCTTCATTCCGAGCCTGCTGCGAAACCTGCTGGAGGAAAGG
CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATTCTCCGCCAACAGCTACTACGGCTACTACGGCTTTTAAAGTCCT
ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCACGCGTTACGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC
CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGCAGCAGTTCTTAAACTGAGTTCTTAAACATCAATCGCGCGGCTTGAGATAGTCAGGCGCG
GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGGGGCTTCTCCGTCACGAAGAGAAAAGTACGCCGGTCATCGACGAGGCAAGATAACCACGCGGAAGCTGAGCAA
ACTGGAGCGAGATAGCGAAGGAGACGCAGGCGAGGCGAGGGTTTGGAGGCAGCAGATAACGGCCAGCAGTACTCAGGGCCGTCAGAATTGTCAGGAAGTCACCGAAAAGCTGAGCAA
GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAAACGCCGAGCTCAAGGCTCCGGAAGGGCGATTCCTTCGAAGGCGTTCGACGAGTTCGACGAAGCACAAGTACGATG
GTTAAAATCGGGCCGGAACTGTGATAAGCTACATCGTTCGATAAGTACATCGTTCTGAAGGGCTCGAAGGGATAGGCGACGAGGCCGTCCCGGACGAGTTCGACGAGCAGCAAGTACGATG
CGGACTACTACATCGAGAACCAGGTTCTGCCGGAACCTCAGGGCCTTCGGCGTACCGCTACCAGAAGACCTGCGCTACCAGAAGACGAGGCGGAGCGCGGCTTGGCGC
GTGGCTGAAGCCGAAGGGGAAGAAGAAGTGA

a

MkTpV   1   valvydaefvgserefeeeretflkGVkAYdgvlaeRYlmeRsssaKRdeELlelhq
RecA   VI   cgnAlkfyasYRidELRigalkdgdEVVg

MkTpV 179   vpIDekeerFleiErenpwtphdELAFrgCLSVeVegekdpessgiyslwsrvvvn
HTH   asnC   IDsidrklInePqkkdgRRisDElAKRVGLSVstVlervlr

HTH   SS   α   α

SEQ. ID. NOS.
73
74

75
76

b

Motif 1   Motif 2

A   299   lkLGdrYGLledvAlcEaraEdgismiattpYEtlkdvc   palteeeAksvnrtl
B   354   atLldehClspdaAdeLlehFeSiagllatdIeiErmYE   eGrlseeAYraavei
C   411   aeLkkeGVGrEtAerLEiraFgnperVkqlareeeiEKLaBVe   eCVGervIrslVpgY
D   468   asLlslrGldrerAerLElkkVYGgYskV   reagvEELrE   dCltdaqTreIkg
E   518   lktLesivgdlekAdeLkrkYGSasaV   rrlpveELrE   lGfSddeTaeTkg
F   568   ipkkLlreafdletAaeLYerYGSlkelg   rrrlsydGNtE   lGatpkaAaeTkgppe
G   622   kfLrnieGVGPElAeLlleavdydieSl   aslnpEElaEVe   lGleeelVyaa
H   696   wkewlerkVGegrArrLleyFGSageVgklvena   evsKRl VpGlCdeaVarlvpg
I   752   ykeLrdaCltpaeAervLkrYGSvskVq   egatpdELrE   lGdakHarllg
J   803   lrBEvnkFldvdtAyeLirkrrYGSvsaV   rkapvkELrE   lGlsdrkHarIkgip
K   855   etmLqvrCmsvekAerHlerFdtwtkV   keapvsELv   VPGVGlslVkeIkaqv
L   912   kaLLdvkGVSpelAdrLVeelGSpyrV   ltakksaLm   VervGPklAerHraag
EcRuvA 73 keLlktnGVGPklAlaLLsgmgaqfV   naverEEvgahpGlGkktAerIivem
HsPolB 57 aeakklpGVGtEiAeLleflatgkllklekir   qddtssiVsGlGpsaArkfvdeg
TaqPol 93 leVmevpGVGpktArgYeaaLGldsle   klkeallergdLl lkcFGakkAerIkegl

Consensus   uu gvg A   ll ygs   u   eu eu gug   u

HhH   SS   α   β   α   α   α   β   α

FIGURE 18   (cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020)

77/78
79/80/81
82
83/84/85
86/87/88
89/90/91
92/93
94/95
96/97/98
99/100/101
102/103/104
105/106/107
108/109
110
111/112/113

FIGURE 19

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAGAGGTAGACATCTCCAA
GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG
CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC
TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEQ ID NO: 121 The amino acid sequence of Sso7d.

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ
MLEKQKK

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCACTAGTCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCC
TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT
GGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT
CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC
CCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTAC
CTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGG
GAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCC
AACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAG
GTGGAGAGGCCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGC
CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC
GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCG
GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA
GACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCG
CGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT
GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCG
CCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTC
CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC
CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG
ATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT
TCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCC
CCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG
GGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTA
CGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG
GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC
CCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT
GCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC
CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG
GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGA
GAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC
CCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC
CAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA

ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP
SNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERPLS
AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF
DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH
PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS
QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV
LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRR
RYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLL
QVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR
GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA
GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC
TTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG
GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG
TGTCACTAGTGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTG
GACGGCCACCACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA
GCCGGGGGGAGCCGGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG
CCCTCAAGGAGGACGGGGACGCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCT
CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCCACGCCAG
AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT
GGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC
CAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG
ACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGGTACCT
CATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGC
CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG
CATCGGGGAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG
CCCTCCTCAAGAACCTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGG
CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT
GCCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG
GGCCTTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG
GAAAGCCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCCGCCGGAAGGGGCCTTC
GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG
CCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCTCA
GGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC
TGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCT
CCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA
GTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAA
CCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGT
GGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGCCT
GGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCCG
CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG
GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG
ACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCGC
GAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG
AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCGCC
TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCG
ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG
GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT
AGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC
CAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCCCC
CGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTACG
AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC

CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGGTACGTGGAGACCC
TCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCC
TGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGCCA
AGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATCATTAA

SEQ ID NO: 125 **The amino acid sequence of Sso7d-Taq fusion protein.**

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA
PKELLQMLEKQKKGGGVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE
PVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQ
LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDR
IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKTARKLL
EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP
DRERLRAFLERLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGFVLSRKEPMWADL
LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA
YLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREV
ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQL
ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL
PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQIRJRRAFIAEEGWLLVA
LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI
NFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL
FGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGA
RMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE
GIDGRGGGGHHHHHH

SEQ ID NO: 126 **The DNA sequence encoding the Pfu-Sso7d fusion protein**

ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT
TCAAAAAAGAGAACGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT
ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC
GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAA
AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAAACTTTATTTGGAACATCCCCAA
GATGTTCCCACTATTAGAGAAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT
TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC
AATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA
TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA
TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA
GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA
GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTCGACTTCCCATAT
TTAGCGAAAAGGGCAGAAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA
AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG
AAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA
TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA
TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT
GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC
CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT
CAAGGTCAAGCACAGGGAACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACG
AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG
CTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCCAGAAAAGGGGTTGTGG
GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC
ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC
TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC

TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT
TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA
AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAAGTACATCGAGTTAGTAT
GGAAGGAGCTCGAAGAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG
GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC
TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA
TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT
AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG
GAGTGAAATTGCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA
CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC
CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC
ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAAACTAGCT
GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA
GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAAA
AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA
CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG
ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC
GGTGGCGGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAGAGGTAGA
CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC
GACGAGGGCGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC
GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERH
GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA
KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID
LPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS
EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI
AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGN
LVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFR
ALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK
MKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIE
LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYE
GFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKETQARVLETILKHGDVEE
AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPG
MVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKED
LRYQKTRQVGLTSWLNIKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGKMIS
FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

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atgattacga attcgacggt gaaggtaaag ttcaagtata aggtgaaga gaaagaagta
gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tggtgtcctt tacctatgac
gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta
gacatgttag caagagcaga aagagagaag aaaggcggcg gtgtcactag ccccaaggcc
ctggaggagg cccctggc ccgccggaa ggggccttcg tgggctttgt gctttcccgc
aaggagccca tgtgggccga tcttctggcc ctggccgccg ccagggggg ccgggtccac
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc
aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccgg cgacgacccc
atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgagggggt ggcccggcgc
tacggcgggg agtggacgga ggaggcgggg gagcgggccg cccttttccga gaggctcttc
gccaacctgt ggggggaggct tgagggggag gagaggctcc tttggcttta ccgggaggtg
gagaggcccc tttccgctgt cctggcccac atggaggcca cggggggtgcg cctggacgtg
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc
ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc
accagcgccg ccgtcctgga ggccctccgc gaggcccacc ccatcgtgga agatcctg
cagtaccggg agctcaccaa gctgaagagc acctacattg acccccttgcc ggacctcatc
```

```
caccccagga cgggccgcct ccacacccgc ttcaaccaga cggccacggc cacgggcagg
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg
atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag
atagagctca gggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag
gaggggcggg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc
gtggacccccc tgatgcgccg ggcggccaag accatcaact tcggggtcct ctacggcatg
tcggcccacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt
gagcgctact ttcagagctt ccccaaggtg cgggcctgga ttgagaagac cctggaggag
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta
gaggcccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag
gaaatggggg ccaggatgct ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa
gagagggcgg aggccgtggc ccggctggcc aaggaggtca tggaggggt gtatcccctg
gccgtgcccc tggaggtgga ggtgggata ggggaggact ggctctccgc caaggagggc
attgatggcc gcggcggagg cgggcatcat catcatcatc attaa
```

SEQ ID NO: 129 **The amino acid sequence of the Sac7d-ΔTaq fusion protein**

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA
PKELLDMLARAEREKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL
AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL
DPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERP
LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV
LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI
HPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDY
SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG
VLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR
RRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARML
LQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDG
RGGGGHHHHHH

SEQ ID NO: 130 **The DNA sequence encoding the PL-ΔTaq fusion protein**

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA
GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA
AGGCGAAGAAAAAGAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG
GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG
CGGTAAGCGAAAAGGACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG
AAAAAGGGCGGCGGTGTCACCAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG
CCGATCTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCG
AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG
ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCC
CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCC
CGGCGCTACGGCGGGGAGTGGACGGAGGAGGCGGGGGAGCGGGCCGCCCTTTCC
GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGAGGCTCCTT
TGGCTTTACCGGGAGGTGGAGAGGCCCCCTTTCCGCTGTCCTGGCCCACATGGAGG
CCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC
CGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTC
AACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC
CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC
TGGAGGCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG
AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC
CAGGACGGGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAG
GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG
CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG
GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAAC
CTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACGGAGACCGCCAGCTGG

ATGTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG
ACCATCAACTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC
TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT
CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGG
GGTACGTGGAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCC
GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCC
AGGGCACCGCCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT
GGAGGAAATGGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA
GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG
AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG
ACTGGCTCTCCGCCAAGGAGGGCATTGATGGCCGCGGCGGAGGCGGGCATCATC
ATCATCATCATTAA

SEQ ID NO: 131 **The amino acid sequence of PL- ΔTaq fusion protein**

MITNSKKKKKKKRKKRKKKKKGGGVTSGATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTSPKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAD
LMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHH

SEQ ID NO: 132 **PRIMER L71F** 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 133 **PRIMER L71R** 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 **PRIMER L18015F** 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 **PRIMER L23474R** 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEQ ID NO: 136 **PRIMER L18015F** 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 **PRIMER L29930R** 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 **PRIMER L30350F** 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 **PRIMER L35121R** 30 5'- CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 **PRIMER L2089F** 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ IUD NO: 141 **PRIMER L7112R** 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 **PRIMER L30350F** 5 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 **PRIMER L40547R** 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 **PRIMER H-Amelo-Y** 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 **PRIMER H-Amelo-YR** 5'-GCTTGAGGCCAACCATCAGAGC-3'

FIGURE 19 (CONT.)

SEQ ID NO: 146 **Human beta-globin primer** 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 **Human beta-globin primer** 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 **Human beta-globin primer** 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

FIGURE 19 (CONT.)

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Figure 20

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

AMINO ACID SEQUENCE (SEQ ID NO: 62)

```
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1               5               10              15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
            20              25              30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35              40              45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50              55              60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65              70              75              80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
            85              90              95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
        100             105             110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115             120             125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130             135             140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145             150             155             160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165             170             175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
        180             185             190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
        195             200             205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260             265             270
```

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```
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
        275             280             285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
        290             295             300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305                 310             315                 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
                325             330             335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
            355             360             365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
    370             375             380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
            420             425             430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
        435             440             445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450             455             460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
            485             490             495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
        515             520             525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545             550             555             560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575
```

FIGURE 20 (CONT.)

```
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
            595             600             605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610             615             620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625             630             635             640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
            645             650             655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
            660             665             670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
            675             680             685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
    690             695             700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705             710             715             720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
            725             730             735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
            740             745             750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
    755             760             765

Trp Leu Asn Ile Lys Lys Ser
    770             775
```

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I

NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

```
ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc      60

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat     120

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag     180

gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga     240

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt     300

taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc     360

aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt     420
```

FIGURE 20 (CONT.)

```
tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta      480

tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt      540

tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct      600

aataccaatg gagggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta      660

tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa      720

tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag      780

cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat      840

agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaaact      900

tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga      960

tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag     1020

gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc     1080

aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga     1140

gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt     1200

ccttccaatg gaaattcagc tttcaagatt agttggacaa cctttatggg atgtttcaag     1260

gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga     1320

agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac     1380

aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt     1440

tagagcccta tatccctcga ttataattac ccacaatgtt tctcccgata ctctaaatct     1500

tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat     1560

ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac     1620

aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc     1680

gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta     1740

ctgtaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg     1800

gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta     1860

tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa     1920

atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag     1980

gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac     2040

tcgtggttta gagatagtta ggagagattg gagtgaaatt gcaaagaaa ctcaagctag     2100

agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga     2160
```

FIGURE 20 (CONT.)

```
agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca    2220

gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa    2280

actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag    2340

aggcgatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca    2400

caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt    2460

ggagggattt ggatacagaa aggaagacct cagataccaa aagacaagac aagtcggcct    2520

aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt    2580

tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta    2640

tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc    2700

tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt    2760

ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct    2820

cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct    2880

tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt    2940

tttgctccaa gcagagccgc tccaatggat aacacccctg ttcccgcacc caagtccgct    3000

acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct    3060

ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg    3120

aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt    3180

taacttttác agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta    3240

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc    3300

ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta    3360

gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa    3420

gtagaagcgg cactactcag atgcttcccc aggaatgagg ttgttgtagc tcntcccnga    3480

aagattgaga tgttcttgg                                                 3499
```

FIGURE 20 (CONT.)